

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: April 24, 2004, 23:54:27 / Search time 1832.72 Seconds
(without alignments)
16460.143 Million cell updates/sec

Title: US-10-051-835-14

Perfect score: 696

Sequence: 1 taaatatctgataggcagt.....ttttgaaaatatataaaat 696

Scoring table: IDENTITY NUC
Gapop 10.0 / Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: GenEmbl.*

- 1: gb_ba.*
- 2: gb_hcg.*
- 3: gb_in.*
- 4: gb_om.*
- 5: gb_ov.*
- 6: gb_pat.*
- 7: gb_ph.*
- 8: gb_pl.*
- 9: gb_pr.*
- 10: gb_ro.*
- 11: gb_sts.*
- 12: gb_sy.*
- 13: gb_vi.*
- 14: gb_vl.*
- 15: em_ba.*
- 16: em_fun.*
- 17: em_hum.*
- 18: em_in.*
- 19: em_mu.*
- 20: em_om.*
- 21: em_or.*
- 22: em_ov.*
- 23: em_pat.*
- 24: em_ph.*
- 25: em_pl.*
- 26: em_ro.*
- 27: em_sts.*
- 28: em_un.*
- 29: em_vi.*
- 30: em_htg_hum.*
- 31: em_htg_inv.*
- 32: em_htg_other.*
- 33: em_htg_mus.*
- 34: em_htg_pln.*
- 35: em_htg_rod.*
- 36: em_htg_mam.*
- 37: em_htg_vrt.*
- 38: em_sy.*
- 39: em_htgo_hum.*
- 40: em_htgo_mus.*
- 41: em_htgo_other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	681.8	98.0	110000	2	AC112773_1	Continuation (2 of
2	681.8	98.0	156043	2	AC013631	AC013631 Homo sapi
3	681.8	98.0	160301	2	AC130417	AC130417 Homo sapi
4	681.8	98.0	178147	2	AC020694	AC020694 Homo sapi
5	681.8	98.0	191246	9	AC068769	AC068769 Homo sapi
6	681.8	98.0	192420	2	AC129804	AC129804 Homo sapi
C 7	89	12.8	7218	6	I66494	I66494 Sequence 14
C 8	52	7.5	134210	9	AC005052	AC005052 Homo sapi
C 9	50	7.2	72968	2	AC115957	AC115957 Mus muscu
C 10	49.8	7.2	221659	2	AC128582	AC128582 Rattus no
C 11	49.8	7.2	263081	2	AC115498	AC115498 Rattus no
C 12	47.6	6.8	128262	9	AL138681	AL138681 Human DNA
C 13	47.2	6.8	143577	9	AC013828	AC013828 Homo sapi
C 14	47.2	6.8	149059	9	AC027779	AC027779 Homo sapi
C 15	47.2	6.8	155185	2	AC074374	AC074374 Homo sapi
C 16	47.2	6.8	181755	2	AC026996	AC026996 Homo sapi
C 17	46.8	6.7	225182	2	AC107742	AC107742 Mus muscu
C 18	46.2	6.6	143501	2	AC125113	AC125113 Mus muscu
C 19	45.8	6.6	227182	2	AC111765	AC111765 Rattus no
C 20	45.2	6.5	168576	2	AC120150	AC120150 Mus muscu
C 21	45.2	6.5	216517	10	AL20415	AL20415 Mus muscu
C 22	45.2	6.5	248577	2	AL845494	AL845494 Mouse DNA
C 23	45.2	6.5	248577	2	AC107771	AC107771 Mus muscu
C 24	45	6.5	73450	2	AC137580	AC137580 Homo sapi
C 25	45	6.5	149041	9	AC044782	AC044782 Homo sapi
C 26	45	6.5	179391	9	AC012558	AC012558 Homo sapi
C 27	45	6.5	179789	9	AC069543	AC069543 Homo sapi
C 28	45	6.5	202050	2	AC060229	AC060229 Homo sapi
C 29	44.8	6.4	9415	6	AX345197	AX345197 Sequence
C 30	44.6	6.4	11391	1	AE011280	AE011280 Leptospir
C 31	44.6	6.4	86734	2	AC144956	AC144956 Silurana
C 32	44.4	6.4	143722	10	AL731792	AL731792 Mouse DNA
C 33	44.2	6.4	74784	9	AL359823	AL359823 Human DNA
C 34	44.2	6.4	92487	10	EX511247	EX511247 Mouse DNA
C 35	44.2	6.4	110000	2	BX572080_2	Continuation (3 of
C 36	44.2	6.4	165358	2	AC009020	AC009020 Homo sapi
C 37	44.2	6.4	186187	9	AC007464	AC007464 Homo sapi
C 38	44.2	6.4	187101	9	AL589862	AL589862 Human DNA
C 39	44.2	6.4	201381	10	AL845491	AL845491 Mouse DNA
C 40	44.2	6.4	211410	2	BX813319	BX813319 Mus muscu
C 41	44	6.3	863	11	CNS06EVQ	AL395628 T7 end of
C 42	43.8	6.3	2000	6	AX655393	AX655393 Sequence
C 43	43.8	6.3	110000	2	BX323883_0	BX323883 Danio rer
C 44	43.8	6.3	110000	2	BX470178_1	Continuation (2 of
C 45	43.8	6.3	152617	2	BX005387	BX005387 Danio rer

ALIGNMENTS

RESULT 1
AC112773_1
WPCOMMENT
Sequence split into 4 fragments LOCUS AC112773 Accession AC112773
Fragment Name Begin End
AC112773_0 1 110000
AC112773_1 100001 210000
AC112773_2 200001 310000
AC112773_3 300001 352840
Continuation (2 of 4) of AC112773 from base 100001 (AC112773 Homo sapiens chromosome 3)

Query Match 98.0%; Score 681.8; DB 2; Length 110000;
Best Local Similarity 99.6%; Pred. No. 2.1e-157;
Matches 694; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

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vector_side:right					
misc_feature					
79490..109959					
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misc_feature					
120437..137338					
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Query Match 98.0%; Score 681.8; DB 2; Length 156043;					
Best-Local Similarity 99.6%; Pred.No. 2e-157;					
Matches 694; Conservative 0; Mismatches 2; Indels 1; Gaps 1;					
Qy	1	TAAATATCTGATAGGCAGTTTGAATAATTGGATTGTGGAAACACAGAGAGAGCGCTTTGATG	60		
Dd	94805	TAAATATCAATAGGCAGTTGAAAAATTGAGTTTGGAAACACAGAGAGAGCGCTTTGATG	94864		
Qy	61	GCGATACACACTTGGAGNACATCAGTCGTGAGCAGTAATGAGATGATTCAGGAAAAGAGT	120		
Dd	94865	GCGATACACACTTGGAGACATCATGTCGTGAGCAGTAATGAGATGATTCAGGAAAAGAGT	94924		
Qy	121	ATAAATCTGGAAAGACACAGAGGACAGGCTCAAAGAACATATTTAAGCACTGGGTAGAAA	180		
Dd	94925	ATAAATCTGGAAAGACACAGAGGACAGGCTCAAAGAACATATTTAAGCACTGGGTAGAAA	94984		
Qy	181	AACAAGAGTAGTAGAACACAGAGTAGGAGATTTATTAGCAGTGACCCTTTGAGAGTACATCT	240		
Dd	94985	AACAAGAGTAGTAGAACACAGAGTAGGAGATTTATTAGCAGTGACCCTTTGAGAGTACATCT	95044		
Qy	241	CTAGAGTCGTATGTGTAGAGCCAGATTTTCAGCATCAGAACCATCAAGCATTTTCGGGGT	300		
Dd	95045	CTAGAGTCGTATGTGTAGAGCCAGATTTTCAGCATCAGAACCATCAAGCATTTTCGGGGT	95104		
Qy	301	GGAAAGAAAGGAGCCATGAATCAAAAGTGGGGAAAAAGGCCCTTTTGGAGGTGSCAGTG	360		
Dd	95105	GGAAAGAAAGGAGCCATGAATCAAAAGTGGGGAAAAAGGCCCTTTTGGAGGTGSCAGTG	95164		
Qy	361	TGGGTAGGGAGTAGGGCTCCGGTTAGAATACATCGATGAAGAAAGGTGAGCACAGCCAT	420		
Dd	95165	TGGGTAGGGAGTAGGGCTCCGGTTAGAATACATCGATGAAGAAAGGTGAGCACAGCCAT	95224		
Qy	421	TTCCCTTTAACACAGAAATACAGATTTCCAGCCCTCTAACCAAGAAACACAAAGTTTGG	480		
Dd	95225	TTCCCTTTAACACAGAAATACAGATTTCCAGCCCTCTAACCAAGAAACACAAAGTTTGG	95284		
Qy	481	GAACATTCCTCTCTCTGAAATATGAAAGAGAGGGGATATAATPACTGGAGTAGGATTGTGA	540		
Dd	95285	GAACATTCCTCTCTCTGAAATATGAAAGAGAGGGGATATAATPACTGGAGTAGGATTGTGA	95344		
Qy	541	AAAAAGTCAAGAG-AAAAAAAAAAGAACAGCCCCAGCTGTAAACAGATACCTTCCATGGAT	599		
Dd	95345	AAAAAGTCAAGAGAAAAAAGAACAGCCCCAGCTGTAAACAGATACCTTCCATGGAT	95404		
Qy	600	GGTAAAAAGGAGTTTTCATATAAATGACCCCTTGGNAGGAGTTCAAAACAGGTTGCC	659		
.Dd	95405	GGTAAAAAGGAGTTTTCATATAAATGACCCCTTGGNAGGAGTTCAAAACAGGTTGCC	95464		
Qy	660	ATATGCTTTATGAGGAGTTTTTGAAAAATATATAAAAT	696		
Dd	95465	ATATGCTTTATGAGGAGTTTTTGAAAAATATATAAAAT	95501		
RESULT 3					
AC130417					
LOCUS					
DEFINITION					
Homo sapiens chromosome 3 clone RP11-12L14, *** SEQUENCING IN					
PROGRESS ***, 15 unordered pieces.					
ACCSSTION					
AC130417					
VERSION					
AC130417.1 GI:22203174					
KEYWORDS					
HTG; HTGS_PHASE1.					


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* 38031 44862: contig of 6832 bp in length
* 44863 44962: gap of 100 bp
* 52959: contig of 7937 bp in length
* 53060 61323: gap of 100 bp
* 61324 72880: contig of 8264 bp in length
* 72881 72980: contig of 100 bp
* 72981 72980: contig of 11457 bp in length
* 72981 72980: gap of 100 bp
* 72981 87502: contig of 14522 bp in length
* 87503 87602: gap of 100 bp
* 104472 104572: contig of 16870 bp in length
* 104573 121407: contig of 100 bp
* 121408 121507: contig of 16835 bp in length
* 121508 139979: contig of 18472 bp in length
* 139980 140079: gap of 100 bp
* 160274 160375: contig of 20195 bp in length
* 160275 160375: gap of 100 bp
* 160375 178147: contig of 17773 bp in length.

FEATURES
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            /db_xref="taxon:9606"
            /chromosome="3"
            /map="3"
            /clone="RP11-637N15"
            /clone_lib="RPC1-11 Human Male BAC"
        1. .1341
            /note="assembly_fragment"
        1442. .2332
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        3033. .4701
            /note="assembly_fragment"
        4802. .6902
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        9988. .12646
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        44963. .52959
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/notes="assembly_fragment"

ORIGIN
Query Match      98.0%; Score 681.8; DB 2; Length 178147;
Best Local Similarity 99.6%; Pred. No. 2e-157;
Matches 694; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

QY 1 TAAATATCTGTAGTGGAGGAGTTCAGAAATTTTGGAAACACAGGAGAGGCTTTTGATG 60
Db 132700 TAAATATCAATAGGCGAGTTAGAAATTTTGGAAACACAGGAGAGGCTTTTGATG 132759
QY 61 GCATACAGACTTTGGAGGACATCAGTCTGAGCAGTAAATAGATCATTCAGGAAAGAGT 120
Db 132760 GCGATACAGACTTTGGAGGACATCAGTCTGAGCAGTAAATAGATCATTCAGGAAAGAGT 132819
QY 121 ATAACTGGGAAGGACAGAGGACAGGCTCAAGGAACATATTTAAGGACTGGTAGAAA 180
Db 132820 ATAACTGGGAAGGACAGAGGACAGGCTCAAGGAACATATTTAAGGACTGGTAGAAA 132879
QY 181 AACAGAGAGTATCAACAGAGTGAGGAGATTTATTAGCAGTGAACCTTTGAGAGTACATCT 240
Db 132880 AACAGAGAGTATCAACAGAGTGAGGAGATTTATTAGCAGTGAACCTTTGAGAGTACATCT 132939
QY 241 CTAGAGTGGTATGTGTAGAGCCAGATTTTCAGCATCAGAACCATCAAGCATTTTGGGGGT 300
Db 132940 CTAGAGTGGTATGTGTAGAGCCAGATTTTCAGCATCAGAACCATCAAGCATTTTGGGGGT 132999
QY 301 GGAAGGAAAAGGAGCCATGAATCAAAAGGTGGGAAAAGGCCCTTTTGGGAGGTGGCAGTG 360
Db 133000 GGAAGGAAAAGGAGCCATGAATCAAAAGGTGGGAAAAGGCCCTTTTGGGAGGTGGCAGTG 133059
QY 361 TGGTAGGGAGTAGGGCTCCGGTTAGAAATACATGGAATGAAGAAGGTGAGCAGCCAT 420
Db 133060 TGGTAGGGAGTAGGGCTCCGGTTAGAAATACATGGAATGAAGAAGGTGAGCAGCCAT 133119
QY 421 TTCCTTTACACAGAAATAACAGATTTCCAGAGCTCTAACCAAGAAACAAACAAGTTTGG 480
Db 133120 TTCCTTTACACAGAAATAACAGATTTCCAGAGCTCTAACCAAGAAACAAACAAGTTTGG 133179
QY 481 GAACATTCCTCTCTCTGAAATATGAAGAAGGGGATTAATACTGGAGTAGGATTTGTA 540
Db 133180 GAACATTCCTCTCTCTGAAATATGAAGAAGGGGATTAATACTGGAGTAGGATTTGTA 133239
QY 541 AAAAAGTCAAGAG-AAAAAAAAGACAGCCCAAGTGTAAACAGATACCTTCTCCATGGAT 599
Db 133240 AAAAAGTCAAGAGAAAAAAAAGACAGCCCAAGTGTAAACAGATACCTTCTCCATGGAT 133299
QY 600 GGTAAAAGGAAGTTATTTCAATAAATGACCCCTTGGAAAGGAGTTCAAAAACAGGTTGCC 659
Db 133300 GGTAAAAGGAAGTTATTTCAATAAATGACCCCTTGGAAAGGAGTTCAAAAACAGGTTGCC 133359
QY 660 ATATGCTTTATGTGGAGTTTGAATAATATATAAAT 696
Db 133360 ATATGCTTTATGTGGAGTTTGAATAATATATAAAT 133396

RESULT 5
AC068769 191246 bp DNA linear PRI 29-JAN-2003
LOCUS Homo sapiens 3 BAC RP11-1412 (Roswell Park Cancer Institute Human
DEFINITION BAC Library) complete sequence.
ACCESSION AC068769
VERSION AC068769.19 GI:27452898
KEYWORDS HTG.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 191246)
AUTHORS Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,P.R., Allen,C.,
Alsbrooks,S.B., Amarutunge,H.C., Are,J.R., Ayele,M., Barks,T.,
Barbaria,J., Benton,J., Binage,K., Blankenburg,K., Bonnin,D.,
Bouck,J., Bowie,S., Brieva,M., Brown,E., Brown,M., Bryant,N.P.,

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Buhay, C., Burch, P., Burkett, C., Burrell, K.L., Byrd, N.C., Carron, T.F., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C., Cleveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R., Davila, M.L., Davis, C., Davy-Carroll, L., Dederich, D.A., Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H., Douthwaite, K.J., Draper, H., Dugan-Rocha, S., Durbin, K.J., Earnhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M., Falls, T., Ferraguto, D., Flagg, N., Ford, J.J., Foster, P., Frantz, P., Gablis, A., Gao, J., Garcia, A., Garner, I., Garza, N., Gill, R., Gorrell, J.H., Guevara, W., Gunaratne, P., Hale, S., Hamilton, K., Harris, C., Harris, K., Hart, M., Havlak, P., Hawes, A., He, X., Hernandez, J., Hernandez, O., Hodgson, A., Hogues, M., Hollway, C., Hollins, B., Homs, F., Howard, S., Huber, J., Hulyk, S., Hume, J., Jackson, L.E., Jacobson, B., Jia, Y., Johnson, R., Jolivet, S., Joudah, S., Karlsson, E., Kelly, S., Khan, U., King, I., Korvah, J., Kovar, C., Kratovic, J., Kresh, A., Landry, N., Leal, B., Lewis, L.C., Lewis, L., Li, J., Li, Z., Lichtarge, O., Lieu, C., Liu, J., Liu, W., Louised, H., Lozano, R.J., Lu, X., Lucier, A., Lucier, R., Luna, R., Ma, J., Maheshwari, M., Mapua, P., Martin, R., Martindale, A., Martinez, E., Massey, E., Mawhney, E., McLeod, M.P., Meador, M., Mei, G., Metzger, M., Miner, G., Miner, Z., Mitchell, T., Mohabbat, K., Moore, S., Morgan, M., Moorish, T., Morris, S., Moser, M., Neal, D., Nelson, D., Newton, J., Newton, N., Nguyen, A., Nguyen, N., Nguyen, N., Nickerson, E., Nwokenko, S., Oguh, M., Okwuonu, G., Oragunye, N., Oviedo, R., Pace, A., Payton, B., Peery, J., Perez, L., Peters, L., Pickens, R., Primus, E., Pu, L.L., Quiles, M., Ren, Y., Rives, M., Rojas, A., Rojubokan, I., Rolfe, M., Ruiz, S., Savery, G., Scherer, S., Scott, G., Shen, H., Shoshitari, N., Sisson, I., Sodergren, E., Sonaite, T., Sparks, A., Stanley, H., Stone, H., Sutton, A., Svatek, A., Tabor, P., Tamerisa, A., Tamerisa, K., Tang, H., Tansey, J., Taylor, C., Taylor, T., Teifrod, B., Thomas, N., Thomas, S., Usmani, K., Vasquez, B., Vera, V., Villalon, D., Vinson, R., Wang, Q., Wang, S., Ward-Moore, S., Warren, R., Washington, C., Watlington, S., Williams, G., Williamson, A., Wleczyk, R., Wooden, S., Worley, K., Wu, C., Wu, Y., Wu, Y.F., Zhou, J., Zorrilla, S., Naylor, S.L., Weinstein, G. and Gibbs, R.

Direct Submission
Unpublished
2 (bases 1 to 191246)
Worley, K.C.

Direct Submission
Submitted (09-MAY-2000) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 191246)
Worley, K.C.

Direct Submission
Submitted (27-SEP-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
4 (bases 1 to 191246)
Worley, K.C.

Direct Submission
Submitted (01-JAN-2003) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
5 (bases 1 to 191246)
Worley, K.C.

Direct Submission
Submitted (29-JAN-2003) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On Jan 1, 2003 this sequence version replaced gi:23334682.
INFORMATION: <http://www.hgsc.bcm.tmc.edu/> or email gc-help@bcm.tmc.edu

CLONE LENGTH: This sequence does not necessarily represent the entire insert of this clone. Overlapping regions of clones are only sequenced and submitted once, so the sequence for the remainder of the insert may be found in the record for the adjacent clones. Overlapping clones are noted at the beginning and end of the Features listing.

ANNOTATION OF FEATURES:

STS are identified using ePCR (Genome Res. 7:541-550) searches of a local database that includes entries from dbSTS, GDB, and local mapping efforts.

Repeats are identified using RepeatMasker (A. Smit and P. Green, unpublished.) for Human and Mouse sequences.

Genes and Region of sequence similarity are identified by BLAST (Nuc. Acids Res. 25:3389-3402) similarity (expect < 1e-34) to the EST and cDNA sequences. Genes demonstrate at least two exons flanked by consensus splice sites that maintained sequence continuity across the splice junctions. Sequences that are not identical matches are annotated as similar.

SEQUENCING READ COVERAGE: Sequencing is completed to a minimum standard of double strand coverage with a minimum of 2 clones and 2 reads with no ambiguities or 2 chemistries with a minimum of 2 clones and 3 reads with no ambiguities. If the sequence quality for a region does not meet this standard, it will be indicated in the annotation as Low Coverage.

QUALITY OF INDIVIDUAL BASES: This sequence meets stringent quality standards - estimated error rate less than 1 per 10,000 bases. Reports of lowest quality individual bases and measures of base quality are listed below. Description of the metrics can be found at URL:

<http://www.hgsc.bcm.tmc.edu:8089/quality.info/genbank.annotation.html>.

FEATURES

Source	Location/Qualifiers
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misc_feature	43..2004 /note="overlaps bases 68997..70958 of clone AC131160" /function="clone overlap" complement(681..843) /rpt_family="MER46C" 844..1121 /rpt_family="AluX" complement(1122..1153) /rpt_family="MER46C" 1154..1511 /rpt_family="L1P8" complement(1512..1580) /rpt_family="MER46C" complement(1638..1751) /rpt_family="MIR" 2318..2617 /rpt_family="AluJb" complement(3530..3695) /rpt_family="L2" 3698..3813 /rpt_family="L1MB6" 3814..4126 /rpt_family="AluSg" 4127..4302 /rpt_family="L1MB6" 4283..5631 /rpt_family="L1MA3" 5632..5643 /rpt_family="AT rich" complement(5644..5936) /rpt_family="AluY" 5937..5956 /rpt_family="AT rich" 5966..6400 /rpt_family="L1MB6" 6401..6695

[illegible]

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TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

Direct Submission
Unpublished
2 (bases 1 to 192420)
Worley,K.C.
Direct Submission
Submitted (03-AUG-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 192420)
Worley,K.C.
Direct Submission
Submitted (27-MAR-2003) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
On Aug 13, 2002 this sequence version replaced gi:22094187.
----- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
----- Project Information
Center Project name: HEJP
Center clone name: RP11-637N16
----- Summary Statistics
Sequencing vector: Plasmid
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 200492 bases at least Q40
Consensus quality: 202310 bases at least Q30
Consensus quality: 203733 bases at least Q20
Estimated insert size: 210002; sum-of-contrigs estimation
Quality coverage: 10x in Q20 bases; sum-of-contrigs estimation

* NOTE: Estimated insert size may differ from sequence length
* (see http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html).
* NOTE: This is a 'working draft' sequence. It currently
* consists of 7 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence.
* As soon as it is available and the accession number will
* be preserved.

*
* 1 2516: contig of 2516 bp in length
* 2517 2616: gap of unknown length
* 2617 4833: contig of 2217 bp in length
* 4834 4933: gap of unknown length
* 4934 13915: contig of 8982 bp in length
* 13916 14015: gap of unknown length
* 14016 36133: contig of 22118 bp in length
* 36134 36233: gap of unknown length
* 36234 80289: contig of 44056 bp in length
* 80290 80389: gap of unknown length
* 80390 127235: contig of 46846 bp in length
* 127236 127336: gap of unknown length
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* 1.192420
* /organism="Homo sapiens"
* /mol_type="genomic DNA"
* /db_xref="taxon:9606"
* /clone="RP11-637N16"

FEATURES
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Location/Qualifiers
1..192420
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ORIGIN
Query Match 98.0%; Score 681.8; DB 2; Length 192420;
Best Local Similarity 99.6%; Pred. No. 2e-157;
Matches 694; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

Qy 1 TAAATATCTGATAGGAGGATTTGAGTTTGGACACAGGAGAGGCTTTGATG 60
Db 111058 TAAATATCAATATAGGAGGATTTGAGTTTGGACACAGGAGAGGCTTTGATG 111117
Qy 61 GCGATACAGACTTGGAGACATCATGCTGCTGAGCAGTAAATGAGATGATTCAGGAAAGAGT 120

111118 GCGATACAGACTTGGAGACATCATGCTGCTGAGCAGTAAATGAGATGATTCAGGAAAGAGT 111177
121 ATAACTGGGAGAGGAGGAGGAGGAGGCTCAAGAGACATATTTAAGGACTGGGTAGAAA 180
111178 ATAACTGGGAGAGGAGGAGGAGGAGGCTCAAGAGACATATTTAAGGACTGGGTAGAAA 111237
181 AACRAGAGAGTATGAACAAGAGTGGAGAGTATTAGCAGTGACCTTTGAGAGTACATCT 240
111238 AACRAGAGAGTATGAACAAGAGTGGAGAGTATTAGCAGTGACCTTTGAGAGTACATCT 111297
241 CTAGAGTGTATGTAGAGCCAGATTTTCAGCATCAGAACCATCAAGCATTTTGGGGGT 300
111298 CTAGAGTGTATGTAGAGCCAGATTTTCAGCATCAGAACCATCAAGCATTTTGGGGGT 111357
301 GGAAGAAAAGGAGCCATGAATCAAAAGGTGGGAAAAGGCGCTTTTGGGAGGTGGCAGTG 360
111358 GGAAGAAAAGGAGCCATGAATCAAAAGGTGGGAAAAGGCGCTTTTGGGAGGTGGCAGTG 111417
361 TGGGTAGGAGTAGGGCTCCGGTTAGATACATGATGATGAAGAGAGTGGAGCAGCAT 420
111418 TGGGTAGGAGTAGGGCTCCGGTTAGATACATGATGATGAAGAGAGTGGAGCAGCAT 111477
421 TTCCTTTACACAGAAATAACAGATTTCCAGCCTCTAACCAAGAAAGCAACAAGTTGG 480
111478 TTCCTTTACACAGAAATAACAGATTTCCAGCCTCTAACCAAGAAAGCAACAAGTTGG 111537
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111538 GAACATTCCTCTCTCTGAAATATGAAGAGAGGGGATTAATCTGAGTAGGATTTGTA 111597
541 AAAAGTCAAGAG-AAAAAAAAGAACAGCCCAAGTGTAAACAGATCTTCCATGGAT 599
111598 AAAAGTCAAGAGAAAAAAAAGAACAGCCCAAGTGTAAACAGATCTTCCATGGAT 111657
600 GTAAAAAGGAGTATTTCATTAATGACCCCTTGAAGAGGTTCAAAACAGGTTGCC 659
111658 GGTAAAAAGGAGTATTTCATTAATGACCCCTTGAAGAGGTTCAAAACAGGTTGCC 111717
660 ATATGCTTTATGTGGAGTTTGAATAATATAAAT 696
111718 ATATGCTTTATGTGGAGTTTGAATAATATAAAT 111754

RESULT 7
I66494/c
LOCUS I66494 7218 bp DNA linear PAT 28-DEC-1997
DEFINITION Sequence 14 from patent US 5670367.
ACCESSION I66494
VERSION I66494.1 GI:2724471
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 7218)
AUTHORS Dörner,F., Scheiflinger,F. and Falkner,F.Gunter.
TITLE Recombinant fowlpox virus
JOURNAL Patent: US 5670367-A 14 23-SEP-1997;
FEATURES Location/Qualifiers
source 1..7218
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Query Match 12.8%; Score 89; DB 6; Length 7218;
Best Local Similarity 4.3%; Pred. No. 2.2e-11;
Matches 17; Conservative 249; Mismatches 129; Indels 0; Gaps 0;

Qy 13 TAGGAGTTAGAAATTTGAGTTTGGACACAGGAGAGGCTTTGATGCGGATACAGACT 72
Db 1462 TAGTTAAAGAGATGAAGATTTGTACRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1403
Qy 73 TGGAGACATCATGCTGCTGAGCAGTAAATGAGATGATTCAGGAAAGAGTATAAATCGGAA 132

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Db      1402 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1343
Qy      133 GAGCAGACGAGCACGGCTCAAGGAACAATATTAAAGACTCGGTAGAAAAACAAGAGAGTA 192
Db      1342 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1283
Qy      193 TGAACAAGAGTGAGGAGATTATTAGCAGTGCACCTTTGAGAGTAGCATCTCTAGAGTCGTAT 252
Db      1282 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1223
Qy      253 GTGTAGAGCCAGATTTTCAGCATCAGAACACATCAAGCATTTTGGGGGTGGAAGAAAAGG 312
Db      1222 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1163
Qy      313 AGCCATCAATCAAAGGTGGGAAAAGGCCCTTTTGGGAGGTGGCAGTGTGGGTAGGGAGT 372
Db      1162 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1103
Qy      373 AGGCTCGGTTAGAATACATGGATGAAGAAGG 407
Db      1102 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1068

RESULT 8
AC005052/c                                linear PRI 08-NOV-2000
LOCUS                                     134210 bp DNA
DEFINITION Homo sapiens BAC clone CTB-38K21 from Xg23, complete sequence.
ACCESSION AC005052
VERSION   AC005052.2 GI:10122134
KEYWORDS
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Sulston,J.E. and Waterston,R.
TITLE    1 (bases 1 to 134210)
JOURNAL  Toward a complete human genome sequence
MEDLINE Genome Res. 8 (11), 1097-1108 (1998)
PUBMED  99063792
REFERENCE 2 (bases 1 to 134210)
AUTHORS Tin-Wollam,A., Graves,T. and Cofman,M.
TITLE    The sequence of Homo sapiens BAC clone CTB-38K21
JOURNAL  Unpublished
REFERENCE 3 (bases 1 to 134210)
AUTHORS Waterston,R.H.
TITLE    Direct Submission
JOURNAL  Submitted (14-SEP-2000) Genome Sequencing Center, Washington
REFERENCE 4 (bases 1 to 134210)
AUTHORS University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA
TITLE    Direct Submission
JOURNAL  Submitted (08-NOV-2000) Department of Genetics, Washington
REFERENCE 5 (bases 1 to 134210)
AUTHORS University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA
TITLE    Direct Submission
JOURNAL  Submitted (14-SEP-2000) Department of Genetics, Washington
COMMENT   On Sep 14, 2000 this sequence version replaced gi:3212939.
          ----- Genome Center
          Center: Washington University Genome Sequencing Center
          Center code: WUGSC
          Web site: http://genome.wustl.edu/gsc
          Contact: sapient@watson.wustl.edu
          ----- Summary Statistics
          Center project name: H RG038K21

```

NOTICE: This sequence may not represent the entire insert of this

clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

MAPPING INFORMATION:

Mapping information:
This sequence was generated from part of bacterial clone contigs of the human chromosome X, constructed by the chromosome X mapping group at the Sanger Centre, Wellcome Trust Genome Campus, Hinxton, UK. Further information can be found at <http://www.sanger.ac.uk/HGP/ChrX/>

SOURCE INFORMATION:

Clone CTB-38K21 is from the first release of the human BAC library CIB-978SK-B. The library contains cloned DNA from the male fibroblast cell line 978SK. See: Shizuya et al., Proc. Natl. Acad. Sci. USA 89:8794-7 (1992); U-J. Kim et al., Genomics 34:213-8 (1996). This clone is available from Research Genetics, Inc. (<http://www.resgen.com>).

VECTOR: pBelobAC11
(http://www.teaggen.

VECTEK: PBIOTBACT
Selection: chloramphenicol

NEIGHBORING SEQUENCE INFORMATION:

NEIGHBORING SEQUENCE INFORMATION:
The clone sequenced to the right is RP3-327A19, 200 base pair overlap. Actual start of this clone is at base position 1 of CTB-38K21; actual end is at base position 9416 of RP3-327A19.

FEATURES

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location/Qualifiers
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/db_xref="taxon:9606"
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/map=Xq23"
/cione="CTB-38K21"
/cione_lfb="CITB-97ASK-B"
20. .268
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repeat_region
269. .561
/rpt_family="Alu"
repeat_region
978. .1285
/rpt_family="Alu"
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6613. .6919
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7154. .7214
/rpt_family="L2"
repeat_region
7640. .7924
/rpt_family="Alu"
repeat_region
8152. .8333
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10586. .10666

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Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schupbach, R.,
Seaman, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N.,
Topham, K., Travers, M., Travis, N., Trigglio, J., Vassiliev, H.,
Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W. J., Young, G.,
Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.

Direct Submission

Submitted (22-MAR-2003) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA

3 (bases 1 to 72968)

REFERENCE

AUTHORS

Birren, B., Nussbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S.,
Barna, N., Bastien, V., Bloom, T., Boguslavskiy, L., Boukhgalter, B.,
Camarata, J., Chang, J., Chazaro, B., Choepel, Y., Collymore, A.,
Cook, A., Cooke, P., Dearellano, K., Dewar, K., Diaz, J. S., Dodge, S.,
Faro, S., Ferreira, P., Fitzgerald, M., Gage, D., Galagan, J.,
Gardyna, S., Gord, S., Graham, L., Grand-Pierre, N., Hafez, N.,
Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C.,
Kamat, A., Karatas, A., Kells, C., Landers, T., Levine, R.,
Lindblad-Toh, K., Liu, G., Maclean, C., Macdonald, P., Major, J.,
Matthews, C., McCarthy, M., Meldrum, J., Meneus, L., Minova, T.,
Ming, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C.,
Norman, C. H., O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J.,
Peterson, K., Phunkhang, P., Pierrel, N., Raymond, C., Retta, R.,
Rise, C., Rogov, P., Roman, J., Roy, A., Schauer, S., Schupbach, R.,
Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N.,
Stojanovic, N., Talamas, J., Tesfaye, S., Theodore, J., Topham, K.,
Travers, M., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X.,
Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.

Direct Submission

Submitted (15-JAN-2003) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA

On Jan 15, 2003 this sequence version replaced gi:25046528.

All repeats were identified using RepeatMasker:

http://ftp.genome.washington.edu/RM/RepeatMasker.html

Smith, A. F. A. & Green, P. (1996-1997)

Center: Genome Center

Center: Whitehead Institute/ MIT Center for Genome Research

Center code: WIBR

Web site: http://www-seq.wi.mit.edu

Contact: sequence.submissions@genome.wi.mit.edu

----- Project Information

Center project name: L24947

Center clone name: 63_E_7

* NOTE: This record contains 68 individual
* sequencing reads that have not been assembled into
* contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely
* arbitrary. Low-pass sequence sampling is useful for
* identifying clones that may be gene-rich and allows
* overlap relationships among clones to be deduced.
* However, it should not be assumed that this clone
* will be sequenced to completion. In the event that
* the record is updated, the accession number will
* be preserved.

1 954: contig of 954 bp in length
* 955 1054: gap of 100 bp
* 1055 2005: contig of 951 bp in length
* 2006 2105: gap of 100 bp
* 2106 3071: contig of 966 bp in length
* 3072 3171: gap of 100 bp
* 3172 4124: contig of 953 bp in length
* 4125 4224: gap of 100 bp
* 4225 5207: contig of 983 bp in length
* 5208 5307: gap of 100 bp
* 5308 6303: contig of 996 bp in length
* 6304 6403: gap of 100 bp
* 6404 7338: contig of 935 bp in length
* 7339 7439: gap of 100 bp
* 7439 8432: contig of 994 bp in length
* 8433 8532: gap of 100 bp
* 8533 9498: contig of 966 bp in length
* 9499 9598: gap of 100 bp

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11647: contig of 964 bp in length
11747: gap of 100 bp
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12806: gap of 100 bp
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13874: gap of 100 bp
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15904: contig of 989 bp in length
16004: gap of 100 bp
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17053: gap of 100 bp
18023: contig of 964 bp in length
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19218: gap of 100 bp
20207: contig of 989 bp in length
20307: gap of 100 bp
21297: contig of 990 bp in length
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22329: contig of 932 bp in length
22429: gap of 100 bp
23445: contig of 1016 bp in length
23545: gap of 100 bp
24478: contig of 933 bp in length
24578: gap of 100 bp
25554: contig of 978 bp in length
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26756: gap of 100 bp
27171: contig of 961 bp in length
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27818: contig of 975 bp in length
28892: gap of 100 bp
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30953: contig of 990 bp in length
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32032: contig of 979 bp in length
32132: gap of 100 bp
33124: contig of 992 bp in length
33224: gap of 100 bp
34237: contig of 1013 bp in length
34337: gap of 100 bp
35339: contig of 1002 bp in length
35439: gap of 100 bp
36449: contig of 1010 bp in length
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37539: contig of 990 bp in length
37639: gap of 100 bp
38621: contig of 982 bp in length
38721: gap of 100 bp
39706: contig of 985 bp in length
39806: gap of 100 bp
40789: contig of 983 bp in length
40889: gap of 100 bp
41795: contig of 906 bp in length
41895: gap of 100 bp
42907: contig of 1012 bp in length
43007: gap of 100 bp
44017: contig of 1010 bp in length
44117: gap of 100 bp
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45194: gap of 100 bp
46189: contig of 995 bp in length
46289: gap of 100 bp
47263: contig of 974 bp in length
47363: gap of 100 bp
48338: contig of 975 bp in length
48438: gap of 100 bp
49412: contig of 974 bp in length

[illegible]

RESULT 10	DNA	linear	HTG 19-SEP-2003
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LOCUS	AC128582		

Rattus norvegicus clone CH230-349P12, *** SEQUENCING IN PROGRESS
***, 2 unordered pieces.
AC128582
AC128582.2 GH:23196069
HTG; HTGS PHASE1; HTGS DRAFT; HTGS_ENRICHED.
Rattus norvegicus (Norway rat)
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.

1 (bases 1 to 221659)
Muzny,D,Marie., Metzker,M.Lee., Abramson,S., Adams,C., Alder,J.,
Allen,C., Allen,H., Alsbrooks,S., Amin,A., Anguiano,D.,
Anyalebechi,V., Aoyagi,A., Ayodeji,M., Baca,E., Baden,H.,
Baldwin,D., Bandaranaike,D., Barber,M., Barnstead,M., Benahmed,F.,
Biswal,N., Blair,J.J., Blankenburg,K., Blyth,P., Brown,M.,
Bryant,N., Buhay,C., Burch,P., Burrell,K., Calderon,E.,
Cardenas,V., Carter,K., Cavazos,I., Ceasar,H., Center,A.,
Chacko,J., Chavez,D., Chen,G., Chen,R., Chen,Y., Chen,Z., Chu,J.,
Cleveland,C., Cockrell,R., Cox,C., Coyle,M., Cree,A., D'Souza,I.,
Davidia,M.L., Davis,C., Davy-Carroll,L., De Anda,C., Dederich,D.,
Delgado,O., Denson,S., Deramo,C., Ding,Y., Dinh,H., Divya,K.,
Draper,H., Dugan-Rocha,S., Dunn,A., Durbin,K., Duval,B., Eaves,K.,
Egan,A., Escotto,M., Eugene,C., Evans,C.A., Falls,T., Fan,G.,
Fernandez,S., Finley,M., Flagg,N., Forbes,L., Foster,M., Foster,P.,
Fraser,C.M., Gabisi,A., Ganta,R., Garcia,A., Garner,T., Garza,M.,
Georgopoulos,E., Geer,K., Gill,R., Grady,M., Guerra,W., Guevara,W.,
Gunaratne,P., Haaland,W., Hamil,C., Hamilton,C., Hamilton,K.,
Harvey,Y., Havlak,P., Hawes,A., Henderson,N., Hernandez,J.,
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Hollins,B., Howles,S., Hulyk,S., Hume,J., Hume,J., Idlebird,D., Jackson,A.,
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Karpathy,S., Kelly,S., Kelly,S., Khan,Z., King,L., Kovar,C.,
Kowis,C., Kraft,C.L., Lebow,H., Levan,J., Lewis,L., Li,Z., Liu,J.,
Liu,J., Liu,W., Liu,Y., London,P., Longacre,S., Lopez,J.,
Lorensuhewa,L., Loulseg,H., Lozado,R.J., Lu,X., Ma,J.,
Maneshwari,M., Mahindaratne,M., Mahmoud,M., Malloy,K., Mangum,A.,
Mangum,B., Mapua,P., Martin,K., Martin,M., Martinez,E.,
Mahoney,S., McLeod,M.P., McNeill,T.Z., Meenen,E.,
Milosavljevic,A., Miner,G., Minja,E., Montemayor,J., Moore,S.,
Morgan,M., Morris,K., Morris,S., Munidas,M., Murphy,M., Nair,L.,
Narkvis,C., Neal,D., Newton,N., Nguyen,N., Norris,S.,
Nwaokaleme,O., Okwuonu,G., Olarnpunsagoon,A., Pal,S., Parks,K.,
Pasternak,S., Paul,H., Perez,A., Perez,L., Pfannkoch,C.,
Plopper,F., Poindexter,A., Popovic,D., Primus,E., Pu,L.,
Puaio,M., Quiroz,J., Rachlin,E., Reeves,K., Regier,M.A., Reigh,R.,
Reilly,B., Reilly,M., Ren,Y., Reuter,M., Richards,S., Riggs,F.,
Rives,C., Rodkey,T., Rojas,A., Rose,M., Rose,R., Ruiz,S.J.,
Sanders,W., Savery,G., Scherer,S., Scott,G., Shatsman,S., Shen,H.,
Shetty,J., Shvartsbeyn,A., Sisson,I., Sitter,C.D., Snajls,D.,
Sneed,A., Sodergren,E., Song,X.-Z., Sorelle,R., Sosa,J.,
Steimle,M., Strong,R., Sutton,A., Svatek,A., Taber,P., Taylor,C.,
Taylor,T., Thomas,N., Thomas,S., Tingey,A., Trejos,Z., Usmani,K.,
Valas,R., Vera,Y., Villanasa,D., Wadron,L., Walker,B., Wang,J.,
Wang,Q., Wang,S., Warren,J., Warren,X., Wei,X., White,F.,
Williams,G., Willson,R., Wlezyk,R., Wooden,H., Worley,K.,
Wright,D., Wright,R., Wu,J., Yakub,S., Yen,J., Yoon,L., Yoon,V.,
yu,F., Zhang,J., Zhou,J., Zhou,X., Zhao,S., Dunn,D., von
Niederhausern,A., Weiss,R., Smith,D.R., Holt,R.A., Smith,H.O.,
Weinstock,G. and Gibbs,R.A.

Direct Submission
2 (bases 1 to 221659)
2 (bases 1 to 221659)
Worley,K.C.

Direct Submission
Submitted (19-JUL-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 221659)
Rat Genome Sequencing Consortium.

Direct Submission
Submitted (19-SEP-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One

Baylor Plaza, Houston, TX 77030, USA

On Sep 19, 2002 this sequence version replaced gi:219039357.
The sequence in this assembly is a combination of BAC based reads
and whole genome shotgun sequencing reads assembled using Atlas
(http://www.hgsc.bcm.tmc.edu/projects/rat/). As a result, the
sequence may extend beyond the ends of the clone and there may be
contigs that consist entirely of whole genome shotgun sequence
reads. Both end sequences and whole genome shotgun sequence only
contigs will be indicated in the feature table.

----- Genome Center of Medicine
Center: Baylor College of Medicine
Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
----- Project Information
Center project name: GYOF
Center clone name: CH230-349P12
----- Summary Statistics
Assembly program: Phrap; version 0.990329
Consensus quality: 204793 bases at least Q40
Consensus quality: 207893 bases at least Q30
Consensus quality: 210176 bases at least Q20
Estimated insert size: 232540; sum-of-contigs estimation
Quality coverage: 3x in Q20 bases; sum-of-contigs estimation

* NOTE: Estimated insert size may differ from sequence length
(see http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html).
* NOTE: This is a 'working draft' sequence.
* consists of 2 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

1 40671: contig of 40671 bp in length
40672 40771: gap of unknown length
40772 221659: contig of 180888 bp in length.
Location/Qualifiers
1. 221659
/organism="Rattus norvegicus"
/mol_type="genomic DNA"
/db_xref="taxon:10116"
/clone="CH230-349P12"

ORIGIN
Query Match 7.2%; Score 49.8; DB 2; Length 221659;
Best Local Similarity 46.8%; Pred. No. 0.079;
Matches 156; Conservative 0; Mismatches 177; Indels 0; Gaps 0;
QY 75 GAGACATCAGCTGACGATTAATGATGATTCAGGAAGGATTAACCTGGGAGA 134
Db 13434 GAGGAGGGGAG 13375
QY 135 GGCAGAGGACAGGCTCAGGAGCAATATTTTAAGGACTGGGTAGAAAAACAAGAGATG 194
Db 13374 AG 13315
QY 195 AACACAGAGTGGAGATTTATAGCAGTGACCTTTTGAGAGTACATCTAGAGTGGTATGT 254
Db 13314 GAG 13255
QY 255 GTAGAGCCAGATTTTTCAGCATCAGAACCATCAAGCATTTTGGGGGTGGAGAAAGGAG 314
Db 13254 GAGGAG 13195
QY 315 CCATGAATCAAAAGTGGGGAGAAAGCCCTTTTGGGAGTGGCGAGTGGGTAGGGATAG 374
Db 13194 AG 13135
QY 375 GGTCCGGTTAGATACATCGATGAGAAAGG 407
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/note="L2 repeat: matches 1667. 1784 of consensus"
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Best local similarity 64.5%; Pred. No. 0.29; Length 126262;
Matches 71; Conservative 0; Mismatches 39; Indels 0; Gaps 0;

QY 2 AAAATATCTGATGGCAGTTAGAAATTTGAGTTGGAAACACAGAGAGAGGCTTTTGATGG 61
Db 30729 AATGTAATCAGTAGGACAGATGATAATATGATGATGATGATGATGATGATGATG 30788
QY 62 CGATACAGACTTGAAGACATACAGTGTGACGAGTAAATGAGATGATCA 111
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RESULT 13
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LOCUS Homo sapiens chromosome, clone RP11-23B7, complete sequence.
DEFINITION AC013828
ACCESSION AC013828.10 GI:15294310
VERSION HTG
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 143577)
Birken,B., Linton,L., Nusbaum,C., Lander,E., Allen,N., Anderson,M.,
Baldwin,J., Barna,N., Beckerly,R., Boguslavsky,L., Bouckgatter,B.,
Brown,A., Castle,A., Collinge,M., Collins,S., Collymore,A.,
Cooke,P., DeArrellano,K., Dewar,K., Domino,L., Donelan,L., Doyle,M.,
Ferreira,P., FitzHugh,W., Forrest,C., Funke,R., Gage,D.,
Galagan,J., Gardyna,S., Grant,G., Hagos,B., Heaford,A., Horton,L.,
Howland,J.C., Johnson,R., Jones,C., Kann,L., Karatas,A., Klein,J.,
Lehoczky,J., Lieu,C., Locke,K., Macdonald,P., Marquis,N.,
McEwan,P., McGurk,A., McKernan,K., McLaughlin,J., Meldrim,J.,
Morrow,J., Naylor,J., Norman,C.H., O'Connor,T., O'Donnell,P.,
Peterson,K., Pollara,V., Riley,R., Roy,A., Santos,R., Severy,P.,
Stange-Thomann,N., Stojanovic,N., Subramanian,A., Talamas,J.,
Tessaye,S., Tirrell,A., Vassiliev,H., Vo,A., Wheeler,J., Wu,X.,
Wyman,D., Ye,W.J., Zimmer,A. and Zody,M.
Direct Submission
Submitted (15-NOV-1999) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
3 (bases 1 to 143577)
Birken,B., Linton,L., Nusbaum,C., Lander,E., Allen,N.,
Anderson,S., Barna,N., Bastien,V., Boguslavsky,L., Bouckgatter,B.,
Brown,A., Canarata,J., Campopiano,A., Chang,J., Chazaro,B.,
Chospel,I., Colangelo,M., Collins,S., Collymore,A., Cook,A.,
Cooke,P., DeArrellano,K., Dewar,K., Diaz,J.S., Dodge,S., Faro,S.,
Ferreira,P., FitzHugh,W., Gage,D., Galagan,J., Gardyna,S.,
Ginde,S., Gord,S., Goyette,M., Graham,L., Grand-Pierre,N.,
Hagos,B., Heaford,A., Horton,L., Hulme,W., Iliev,I., Johnson,R.,
Jones,C., Kamat,A., Karatas,A., Kells,C., LaRocque,K.,
Lamazzes,R., Landers,T., Lehoczky,J., Levine,R., Liu,G.,
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Raymond,C., Retta,R., Riback,M., Riley,R., Rise,C., Rogov,P.,
Roman,J., Rosetti,M., Roy,A., Santos,R., Schauer,S., Schuback,R.,
Seaman,S., Severy,P., Spencer,B., Stange-Thomann,N., Stojanovic,N.,
Strauss,N., Subramanian,A., Talamas,J., Tessaye,S., Theodore,J.,

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Topham,K., Travers,M., Travis,N., Trigilio,J., Vassiliev,H.,
 Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G.,
 Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.
 Direct Submission
 Submitted (04-SEP-2001) Whitehead Institute/MIT Center for Genome
 Research, 320 Charles Street, Cambridge, MA 02141, USA
 On Aug 27, 2001 this sequence version replaced gi:14547834.
 All repeats were identified using RepeatMasker:
 Smit,A.P.A. & Green, P. (1996-1997)
 http://ftp.genome.washington.edu/RM/RepeatMasker.html
 ----- Genome Center

Center: Whitehead Institute/ MIT Center for Genome Research
 Center code: WBIR
 Web site: http://www-seq.wi.mit.edu
 Contact: sequence submissions@genome.wi.mit.edu

----- Project Information

Center project name: L4171
 Center clone name: 23_B_7

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Db 125704 CCAGCTAACATATAAAGAAACTTGGATATTCGAACACTTCAAGAGAAAGTAGGAAAGA 125763
QY 516 GATAAATACTGGAGTAGGATTGTGAAAAAGTCAAGAGAAAAAAGAAAAAGAACAGCCCAAGT 575
Db 125764 GAAAAAATACATGGACACAGAGAAGAAATCTTAATCATATAAATTAACCCCAAT 125823
QY 576 GTAAACAGATATCTCCATGGATGGTAAAGAAAGATTATTTCAATAAATGACCCCTT 635
Db 125824 GTATCAGTTA-TTATAATGAAATGAATTAATGCTCTGATTAATAAATAAAGATTACTA 125882
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RESULT 14
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DEFINITION AC027779
ACCESSION AC027779.10 GI:18182811
VERSION HTG.
KEYWORDS SOURCE
ORGANISM Homo sapiens (human)
REFERENCE 1 (bases 1 to 149059)
AUTHORS Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N.,
TITLE Anderson,S., Baldwin,J., Barna,N., Bastien,V., Bada,P.,
JOURNAL Boguslavskiy,L., Boukhgalter,B., Brown,A., Burkett,G.,
REFERENCE Campopiano,A., Castle,A., Cheepel,Y., Colangelo,M., Collins,S.,
AUTHORS Dodge,S., Domino,M., Doyle,M., Ferreira,P., FitzHugh,W.S., Gage,D.,
Boguslavskiy,L., Boukhgalter,B., Brown,A., Burkett,G.,
Dodge,S., Domino,M., Doyle,M., Ferreira,P., FitzHugh,W.S., Gage,D.,
Galan,J., Gardyna,S., Ginde,S., Goyette,M., Graham,L.,
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Levine,R., Lieu,C., Liu,G., Locke,K., Macdonald,P., Marcuis,N.,
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Meldrum,J., Meneus,L., Mihova,T., Miranda,C., Mlenga,V., Morrow,J.,
Murphy,T., Naylor,J., Norman,C.H., O'Connor,T., O'Donnell,P.,
O'Neil,D., Oliver,T.M., Oliver,J., Peterson,K., Pierre,N.,
Pisani,C., Pollara,V., Raymond,C., Riley,R., Rogov,P., Rothman,D.,
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Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J.,
Young,G., Zainoun,J., Zimmer,A. and Zody,M.
Direct Submission
Submitted (01-APR-2000) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
3 (bases 1 to 149059)
AUTHORS Birren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N.,
Anderson,S., Barna,N., Bastien,V., Boguslavskiy,L., Boukhgalter,B.,
Brown,A., Camarata,J., Campopiano,A., Chang,J., Chazaro,B.,
Choepe,Y., Colangelo,M., Collins,S., Collymore,A., Cook,A.,
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Best Local Similarity 52.5%; Pred. No. 0.35;
Matches 126; Conservative 0; Mismatches 113; Indels 1; Gaps 1;

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Db 20779 GTATCACTTA-TTATAATGAATGAATTAATGCTCTGATTAATAAATAAGATTACTA 20837

Qy 636 GGAAGGAGTTCAAAACACAGTTGTCATATGCTTTATGAGGAGTTTGAATAATATAAAA 695
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RESULT 15
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LOCUS Homo sapiens chromosome 11 clone RP11-651C3, WORKING DRAFT
DEFINITION AC074374
ACCESSION AC074374
VERSION AC074374.3 GI:9887833
KEYWORDS HTG; HTGS_Phrase1; HTGS_DRAFT.
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 155185)
AUTHORS Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE The sequence of Homo sapiens clone
JOURNAL Waterston,R.H.
REFERENCE 2 (bases 1 to 155185)
AUTHORS Waterston,R.H.
TITLE Direct Submission
JOURNAL Submitted (29-JUL-2000) Genome Sequencing Center, Washington
University School of Medicine, 444 Forest Park Parkway, St. Louis,
MO 63108, USA
COMMENT On Aug 24, 2000 this sequence version replaced gi:9795994.

----- Genome Center -----
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: http://genome.wustl.edu/gsc/index.shtml
----- Project Information -----
Center project name: H.NH0651C03
----- Summary Statistics -----
Sequencing vector: M13; 100%
Chemistry: Dye-primer ET; 100% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 145940 bases at least Q40
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Insert size: 157000; agarose-fp
Insert size: 153085; sum-of-contigs
Quality coverage: 4.43 in Q20 bases; agarose-fp
Quality coverage: 4.61 in Q20 bases; sum-of-contigs
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* NOTE: This is a 'working draft' sequence. It currently
* consists of 22 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
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* 1 2478: contig of 2478 bp in length
* 2479 2578: gap of unknown length
* 2579 4930: contig of 2352 bp in length
* 5031 5030: gap of unknown length
* 5031 7763: contig of 2733 bp in length
* 7764 7863: gap of unknown length
* 7864 11285: contig of 3422 bp in length
* 11286 11385: gap of unknown length
* 11386 14925: contig of 3540 bp in length
* 14926 18227: gap of unknown length
* 18228 18327: contig of 3202 bp in length
* 18328 23954: gap of unknown length
* 23955 26074: contig of 4020 bp in length
* 26075 26174: gap of unknown length
* 26175 30628: contig of 4454 bp in length
* 30629 30728: gap of unknown length
* 30729 35614: contig of 4886 bp in length
* 35615 35714: gap of unknown length
* 35715 42284: contig of 6569 bp in length
* 42285 42383: gap of unknown length
* 42384 49108: contig of 6725 bp in length
* 49109 49208: gap of unknown length
* 49209 55858: contig of 6650 bp in length
* 55859 55958: gap of unknown length
* 55959 65238: contig of 9280 bp in length
* 65239 65338: gap of unknown length
* 65339 75264: contig of 9926 bp in length
* 75265 75365: gap of unknown length
* 75366 91540: contig of 16175 bp in length
* 91541 91640: gap of unknown length
* 91641 111316: contig of 19677 bp in length
* 111317 111416: gap of unknown length
* 111417 147337: contig of 36021 bp in length
* 147338 147537: gap of unknown length
* 147538 148789: contig of 1252 bp in length
* 148790 148890: gap of unknown length
* 148891 150390: contig of 1501 bp in length
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[illegible]

Search completed: April 25, 2004, 18:58:05
Job time : 1841.72 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model
Run on: April 25, 2004, 07:00:48 ; Search time 6359.53 Seconds
(without alignments)
16458.288 Million cell updates/sec

Title: US-10-051-835-13
Perfect score: 3505
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
Searched: 27513289 seqs, 14931090276 residues
Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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1:	em_estba:*
2:	em_estum:*
3:	em_estin:*
4:	em_estmu:*
5:	em_estov:*
6:	em_estpl:*
7:	em_estro:*
8:	em_hci:*
9:	gb_est1:*
10:	gb_est2:*
11:	gb_hic:*
12:	gb_est3:*
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27:	em_gss_vrl:*
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29:	gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	1771.2	50.5	3206	11	AK077976 Mus muscu
3	1767	50.4	2133	29	AY402622 Pan trogl
4	1700.2	48.5	3086	11	AK035918 Mus muscu

5	1370.6	39.1	2172	29	AY402623
6	952.2	27.2	1114	13	EX367242
C	929.4	26.5	1201	13	EX363741
C	876	25.0	922	13	EX350606
9	856.6	24.4	926	13	EX350606
10	849.2	24.2	1201	13	EX384966
11	827.4	23.6	974	13	EX384966
12	823.8	23.5	960	13	EX390196
13	775	22.1	801	13	EX112994
C	772.2	22.0	797	14	CB243787
16	768	21.9	912	13	BO883972
17	759.2	21.7	892	14	EX376660
18	748.6	21.4	951	13	CD107028
19	708.6	20.2	917	14	BO056228
20	698.2	19.9	775	9	CA454892
21	689.6	19.7	970	13	AU122156
22	681	19.4	1066	12	BO707628
23	673	19.2	1090	13	EM806752
24	661.8	18.9	666	12	EX367243
25	655	18.7	666	12	EX367243
26	650	18.5	925	13	BO884636
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34	579.2	16.5	720	14	BU686374
35	551.4	15.7	695	12	BO632880
36	550.8	15.6	709	13	BO960065
37	546.6	15.5	547	12	BI683727
38	543.4	15.4	547	12	BO573544
39	540.8	15.4	667	12	BO573544
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41	537	15.3	841	14	BO703963
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43	527.8	15.1	528	14	CB566426
44	524.6	15.0	944	12	CA393520
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					CR022938

ALIGNMENTS

RESULT 1	AY402621	2172 bp	DNA	linear	GSS 12-DBS-2003
LOCUS	Homo sapiens HCM1285 gene, VIRTUAL TRANSCRIPT, partial sequence,				
DEFINITION	Genomic survey sequence.				
ACCESSION	AY402621.1	GI:39758607			
VERSION	AY402621.1	GI:39758607			
KEYWORDS	GSS.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
REFERENCE	1 (bases 1 to 2172)				
AUTHORS	Clark, A.G., Gnanowski, S., Nielson, R., Thomas, P., Kejarawal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferreria, S., Wang, G., Zheng, X.H., White, T.J., Shinsky, J.J., Adams, M.D. and Cargill, M.				
TITLE	Inferring nonneutral evolution from human-chimp-mouse orthologous gene trics				
JOURNAL	Science 302 (5652), 1960-1963 (2003)				
PUBMED	14671302				
REFERENCE	2 (bases 1 to 2172)				
AUTHORS	Clark, A.G., Gnanowski, S., Nielson, R., Thomas, P., Kejarawal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferreria, S., Wang, G., Zheng, X.H., White, T.J., Shinsky, J.J., Adams, M.D. and Cargill, M.				
TITLE	Direct Submission				

JOURNAL	Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA									
COMMENT	This sequence was made by sequencing genomic exons and ordering them based on alignment.									
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	Matches 1873;	Conservative	0;	Mismatches	299;	Indels	0;	Gaps	0;	
Qy	204	ATGGCCCTCCAGCCCTCGGCGCTGGACCCCTGAGCCTCTGGGCTTTCTCTTCCAA	263							
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Qy	264	CTGCTTCAGCTGCTGTCGCGACGACGCCGCGGGGAGCGGGCGAGGGCCCATGCC	323							
Db	61	CTGCTTCAGCTGCTGTCGCGACGACGCCGCGGGGAGCGGGCGAGGGCCCATGCC	120							
Qy	324	AGGCTCAGATACATGACAGGGGATGACGTAGGCACTTAGCTTCTCCACCAAGAGGC	383							
Db	121	AGGCTCAGATACATGACAGGGGATGACGTAGGCACTTAGCTTCTCCACCAAGAGGC	180							
Qy	384	CTCCAGGATTTGACACTCTGCTCTGAGTGGTGAATGGAATAACTCTCTACGTGGGGCT	443							
Db	181	CTCCAGGATTTGACACTCTGCTCTGAGTGGTGAATGGAATAACTCTCTACGTGGGGCT	240							
Qy	444	CGAAGCCATTCGGCTTGGATATCCAGGATCCAGGGTCCCGAGGCTTAAAGAACATG	503							
Db	241	CGAAGCCATTCGGCTTGGATATCCAGGATCCAGGGTCCCGAGGCTTAAAGAACATG	300							
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Qy	624	ACCTGGGCACTTCGGCTTCAGCCCTGCTGATACCTTCAATTTCAAGATTCCTAC	683							
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Db	781	NN	840							

Qy	1044	AAGAAGTGGACCACTTCTCTGAAGGCCAGCTGCTCTGCAACCCAGCGGGGAGCTGCC	1103							
Db	841	NN	900							
Qy	1104	TTCAACGTCATCCGCCACGCGCTCTGCTCCCGCGGATCTCCACAGCTCCCCACATC	1163							
Db	901	NN	960							
Qy	1164	TACGACGCTTTCACCTCCAGTGGCGGGACGAGGAGCTCTCGGCTTTGTGCC	1223							
Db	961	NN	1020							
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Db	1201	CAAGTGGTGGGACGCGCCCTGCTGGTGAATCTGGCGTGGAGTATACACGGCTTGCAGTG	1260							
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Db	1741	CCCAACCTGTGAGCTTGGCTCTTTATTTATGGAGTCTATGGCCCGCAGCAGCTCCAGAA	1800							
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1921 GACAGCAGCAGCAGCAGCCTGGCCCTGGATCTCTAAGTGGCGAGCATCCCCGGGAGCAT 1980
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RESULT 2
AK077976
LOCUS      3206 bp      mRNA      linear      HTC 18-SEP-2003
DEFINITION Mus musculus 13 days embryo male testis cDNA, RIKEN full-length
              enriched library, clone:6030492A12 product:sema domain,
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              cytoplasmic domain, (semaphorin) 4A, full insert sequence.
ACCESSION  AK077976
VERSION     AK077976.1 GI:26097602
KEYWORDS   HTC; CAP trapper.
SOURCE     Mus musculus (house mouse)
ORGANISM   Mus musculus

REFERENCE  1
AUTHORS   Carninci, P. and Hayashizaki, Y.
TITLE     High-efficiency full-length cDNA cloning
JOURNAL   Meth. Enzymol. 303, 19-44 (1999)
MEDLINE   99279253
PUBMED    10349636
REFERENCE  2
AUTHORS   Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
              Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
TITLE     Normalization and subtraction of cap-trapper-selected cDNAs to
              prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL   Genome Res. 10 (10), 1617-1630 (2000)
MEDLINE   20499374
PUBMED    11042159
REFERENCE  3
AUTHORS   Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,
              Konno, H., Akiyama, J., Nishi, K., Kitsuunai, T., Tashiro, H., Itoh, M.,
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              Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,
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              Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J.,
              Okazaki, Y., Muramatsu, M., Inoue, Y., Kizawa, A. and Hayashizaki, Y.
TITLE     RIKEN integrated sequence analysis (RISA) system--384-format
              sequencing pipeline with 384 multipeppillary sequencer
JOURNAL   Genome Res. 10 (11), 1757-1771 (2000)
MEDLINE   20530913
PUBMED    11076861
REFERENCE  4
AUTHORS   The RIKEN Genome Exploration Research Group Phase II Team and the
              FANTOM Consortium.
TITLE     Functional annotation of a full-length mouse cDNA collection
JOURNAL   Nature 409, 685-690 (2001)
MEDLINE   11076861
PUBMED    11076861
REFERENCE  5
AUTHORS   The FANTOM Consortium and the RIKEN Genome Exploration Research
              Group Phase I & II Team.
TITLE     Analysis of the mouse transcriptome based on functional annotation
              of 60,770 full-length cDNAs
JOURNAL   Nature 420, 563-573 (2002)
MEDLINE   11076861
PUBMED    11076861

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AUTHORS  Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P.,
              Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K.,
              Hayashida, N., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, F.,
              Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Kato, H.,
              Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S.,
              Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M.,
              Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y.,
              Saigo, R., Saichoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H.,
              Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y.,
              Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y.,
              Tanaka, T., Tomaru, A., Toyota, T., Yasunishi, A., Muramatsu, M. and
              Hayashizaki, Y.
TITLE     Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of
              Physical and Chemical Research (RIKEN), Laboratory for Genome
              Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
              RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
              Kanagawa 230-0045, Japan (E-mail: genome-res@gsc.riken.go.jp,
              URL: http://genome.gsc.riken.go.jp/, Tel: 81-45-503-9222,
              Fax: 81-45-503-9216)
COMMENT   cDNA library was prepared and sequenced in Mouse Genome
              Encyclopedia Project of Genome Exploration Research Group in Riken
              Genomic Sciences Center and Genome Science Laboratory in RIKEN.
              Division of Experimental Animal Research in Riken contributed to
              prepare mouse tissues.
              Please visit our web site for further details.
              URL: http://genome.gsc.riken.go.jp/
              URL: http://fantom.gsc.riken.go.jp/.
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Qy	1021	TGGGCGGGAAGAGCTGTGAGAGAGTGAAGACCATCTTCTGTAAGGCCACAGTGTCT	1080
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1581 GTGCTTATCTGTGGAGAGATTACAGCTGAGCCCTGACTCTGAGCCTGTTCGAAACCTG 1640

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Qy 2518 CAGGACCTGGCATGCTGGCTGGCGGCCCAAGCAGACGCCCTGACTAGGATGACACGAG 2577
Db 2538 CAGGCACTGGCTTGTGGCTATGC-----CAG 2566
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Db 2567 GCACAGTGCCACTCTGACAGGCTAGGAGGCTCTCTGCTAACGTGTGTCACTACAGCA 2626
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Qy 3222 AAAA 3225
Db 3185 AAAA 3188

RESULT 3
AY402622
LOCUS
DEFINITION
Pan troglodytes HCM1285 gene, VIRTUAL TRANSCRIPT, partial sequence,
genomic survey sequence.
ACCESSION
AY402622
VERSION
AY402622.1
KEYWORDS
GSS.
SOURCE
Pan troglodytes (chimpanzee)
ORGANISM
Pan troglodytes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
REFERENCE
1 (bases 1 to 2133)
AUTHORS
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A.,

Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Shinsky, J.J.,
Adams, M.D. and Cargill, M.
Inferring nonneutral evolution from human-chimp-mouse orthologous
gene trios
Science 302 (5652), 1960-1963 (2003)
JOURNAL
PUBMED
14671302
REFERENCE
AUTHORS
2 (bases 1 to 2133)
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A.,
Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Shinsky, J.J.,
Adams, M.D. and Cargill, M.
Direct Submission
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering
them based on alignment.
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/mol_type="genomic DNA"
/db_xref="taxon:9598"
gene
1..2133
/locus_tag="HCM1285"
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Best Local Similarity 83.0%; Pred. No. 0;
Matches 1770; Conservative 0; Mismatches 363; Indels 0; Gaps 0;
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Db 1 ATGGCCCTCCAGCCCTGGGCTTGACCCCTGGAGGCTCTGGGCTTTCTCTTCCAA 60
Qy 264 CTGCTTCAGCTGTCTGCTGCCAGCAGACCGCGGGGGAGGGGCGGCGGCGGCGGCGG 323
Db 61 CTGCTTCAGCTGTCTGCTGCCAGCAGCAGCGCGGGGGAGGGGCGGCGGCGGCGGCGG 120
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Qy 384 CTCAGGATTTTGACACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 443
Db 181 CTCAGGATTTTGACACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
Qy 444 CGAGAGCCATTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 503
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Qy 504 ATACCGTGGCCAGCCAGTCACAGAAAGAGTGAATGTCCTTTAAGAGAGAGCAAT 563
Db 301 ATACCGTGGCCAGCCAGTCACAGAAAGAGTGAATGTCCTTTAAGAGAGAGCAAT 360
Qy 564 GAGACACAGTGTTCACCTTCATCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 623
Db 361 GAGACACAGTGTTCACCTTCATCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420
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Db 541 GCTCAGACATACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600
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QY 1584 CAGCTGTTCCTGACCTGACCTGTTCCGCACTGACGCTGGCGCCCGCCAGGCTGCA 1643
DB 1381 CAGCTGTTCCTGACCTGACCTGTTCCGCACTGACGCTGGCGCCCGCCAGGCTGCA 1440
QY 1644 GTGTTGTAGGCTTCTCAGGAGGTGTCTGGAGGCTGCCCGAGCAACTGTAGTGTCTAT 1703
DB 1441 GTGTTGTAGGCTTCTCAGGAGGTGTCTGGAGGCTGCCCGAGCAACTGTAGTGTCTAT 1500
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QY 1764 CGAACCTGTGCTCTCTCTGCCCCCAACTGAACTCTCTGGAAGCAGGACATGGAGCGG 1823
DB 1561 CGAACCTGTGCTCTCTCTNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 1620
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QY 2064 CTCTACCAAGTGTGGGCAACTGAGAAATGGCTTTTCATACCTGTGATCTCTACTTGGGTG 2123
DB 1861 CTCTACCAAGTGTGGGCAACTGAGAAATGGCTTTTCATACCTGTGATCTCTACTTGGGTG 1920
QY 2124 GACAGCCAGGACGACGACCTGGCCCTGGATCTGAACTGGCAGGACATCCCGGGAGCAT 2183
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QY 2184 GTGAAGGTCCCGTTCACAGGCTCAGTGGTGGGCGCGCTGGCTGCCACGAGTCCCTAC 2243
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QY 2244 TGGCCCGCACTTTGTGTCACGTGTCTCTCTCTTTGCTTGTGCTTTAGGAGCCCTCATC 2303
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QY 2304 ATCTCTCGTGGCTCCCGCTTCCGATTCAGAGCACTCCGG 2336
DB 2101 ATCTCTGTTGGCTCCCGCTTCCGATTCAGAGCACTCCGG 2133

RESULT 4
AK035918 3086 bp mRNA linear HTC 19-SEP-2003
LOCUS Mus musculus 16 days neonate cerebellum cDNA, RIKEN full-length
DEFINITION enriched library, clone:9630018D15 product:sena domain,
immunoglobulin domain (Ig), transmembrane domain (TM) and short
cytoplasmic domain, (semaphorin) 4A, full insert sequence.
ACCESSION AK035918
VERSION AK035918.1 GI:26084904
KEYWORDS HTC; CAP trapper.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1
REFERENCE
AUTHORS Carninci,P. and Hayashizaki,Y.
TITLE High-efficiency full-length cDNA cloning
JOURNAL Meth. Enzymol. 303, 19-44 (1999)
MEDLINE 99279253
PubMed 10349636
2
REFERENCE
AUTHORS Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
TITLE Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL Genome Res. 10 (10), 1617-1630 (2000)
MEDLINE 20499374
PubMed 11042159
3
REFERENCE
AUTHORS Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,
Konno,H., Akiyama,J., Nishi,K., Kitsuai,T., Tashiro,H., Itoh,M.,
Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A.,
Yanamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K.,
Fujiwaki,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Wataiki,M.,
Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsura,S., Kawai,J.,
Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
TITLE RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer
JOURNAL Genome Res. 10 (11), 1757-1771 (2000)
MEDLINE 20530913
PubMed 11076861
4
REFERENCE
AUTHORS The RIKEN Genome Exploration Research Group Phase II Team and the
FANTOM Consortium.
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Db 1226 CGAGGCCAGGAGTTGCTCCATGGGCCCTTCTCTGACAAAGCTTGACCTTCATGAGG 1285
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RESULT 5
AY402623

LOCUS 2172 bp DNA linear GSS 12-DEC-2003
DEFINITION Mus musculus HCM1285 gene, VIRTUAL TRANSCRIPT, partial sequence,
genomic survey sequence.

ACCESSION AY402623

VERSION AY402623.1 GI:39758609

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Euthera; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 2172)

Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarival, A.,

Todd, M.A., Tanenbaum, D.M., Civallo, D.R., Lu, F., Murphy, B.,

Ferrera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,

Adams, M.D. and Cargill, M.

Inferring nonneutral evolution from human-chimp-mouse orthologous

TITLE


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QY 2004 GCCTCTTCCACTGCTCAATGGCTCCCTCTTGCTGATAGTGCAGGATGGAGTTGGGGT 2063
| | | | |
Db 1801 GCCTCTGCTACCGCTACATGGCTCCCTCTTGCTGCTCGGAGAGATGGTGTGCGGGGC 1860
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QY 2064 CTCTACCAAGTCTGGGCAACTGAGAAAGGCTTTTATACACCTGTGATCTCTACTGGGTG 2123
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Db 2161 ATGCTGCCCC 2171
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RESULT 6
BX367242/c
LOCUS
DEFINITION BX367242 Homo sapiens B CELLS (RAMOS CELL LINE) COT 25-NORMALIZED
Homo sapiens cDNA clone CS0DL002Y004 3-PRIME, mRNA sequence.
ACCESSION BX367242
VERSION
KEYWORDS
SOURCE EST.
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1114)
AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 907.f For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0AL002BH02NPI&cluster=907.f. Contact :
Peng Liang Email: fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ invitrogen Corporation 1600
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25-NORMALIZED"
/notes="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."

FEATURES
source
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Query Match 27.2%; Score 952.2; DB 13; Length 1114;
Best Local Similarity 94.9%; Pred. No. 3.2e-225; Indels 4; Gaps 4;
Matches 997; Conservative 24; Mismatches 26;

QY 2172 CCCCGGAGCATGTGAAGGTCCTCCCTTTGACCCAGGGTCAAGTGTGGGGCGCCCTGGCTGCC 2231
| | | | |
Db 1055 CCCCGGAGCATGTGAAGTCCCTTTCACMAGGGTCAAGTGG-KGGGCGGCCCTGGCTGCC 998
| | | | |
QY 2232 CAGCAGTCTTACTTGGCCCC-ACCTTGTCACTGTCACTGTCTCTTTCCTTTCCTTTCCTTTC 2290
| | | | |
Db 997 CAGCAGTCTTACTTGGCCCCAACCTTTGAACTGTAACTGTCTCTTTCCTTTCCTTTCCTTTC 938
| | | | |
QY 2291 AGGAGCCCTCATCATCTCTGCTGSCCTCCCC-ATTGAGAGCACTCCGGGCTCGGGGCAAGG 2349
| | | | |
Db 937 AGGAGCCCTCATCATCTCTGCTGSCCTCCCCAATTGAGAGMACCTCCGGGCTCGGGCGCAAGG 878
| | | | |
QY 2350 TTCAGGGCTGTGAGACCTCGCCCTGGGAGAGAGCCCGCTTAAGCAGAGAGCAACACC 2409
| | | | |
Db 877 TTMAGGGCTGTGAGACCTCGCCCTGGGAGAGAGCCCGCTTAAGCAGAGAGCAACACC 818
| | | | |
QY 2410 TCCAGTCTCCCAAGGAATGCAGGACCTCTGCGAGTGTGGAGCGCTGACAAACAACCTGCC 2469
| | | | |
Db 817 TCCAGTCTCCCAAGGAATGCAGGACCTCTGCGAGTGTGGAGCGCTGACAAACAACCTGCC 758
| | | | |
QY 2470 TAGGCACTGAGGTAGCTTAACTCTAGGCACAGSCCGGGCTGGGTGCAGGACCTGGC 2529
| | | | |
Db 757 TAGGCACTGAGGTAGCTTAACTCTAGGCACAGSCCGGGCTGGGTGCAGGACCTGGC 698
| | | | |
QY 2530 CATGCTGGCTGGCGGCCCAAGCACAGCCCTGACTAGGATGACAGCAGCAGCAAAAGACCA 2589
| | | | |
Db 697 CATGCTGGCTGGCGGCCCAAGMACAGCCCTGACTAGGATGACAGCAGCAGCAAAAGACCA 638
| | | | |
QY 2590 CTTTCTCCCTGAGAGAGGCTTCTGCTACTGCTCACTGATGACACTCAGCAGAGGCTG 2649
| | | | |
Db 637 CTTTCTCCCTGAGAGAGGCTTCTGCTACTGCTCACTGATGACACTCAGCAGAGGCTG 578
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Db 577 ATGCACAGCAGTCTGCTCCCTATGGAGCTCCCTTCTACCAAGCACATGAGCTCTCTAA 518
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QY 2710 CAGGGTGGGGCTACCCCGCAGACCTGCTCTCACTGATATTGAAGAACCTGAGAGGAT 2769
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QY 2770 CTTTCAGTTCTGGGCATTTCAGGAGACCTCCAGAAAACACAGTGTTCACAGAGACCTTAAA 2829
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| | | | |
QY 2830 AAACCTGCTGTCCTCCAGGACCTTATGTAATGAACACCAACATCTTAAACAATATATGC 2889
| | | | |
Db 397 AAACCTGCTGTCCTCCAGGACCTTATGTAATGAACACCAACATCTTAAACAATATATGC 338
| | | | |
QY 2890 TAACATGCCACTCTCGAAAACCTCCACTCTGAAGCTCGCGTTTGGACACCAACCTCCCT 2949
| | | | |
Db 337 TAAATGCACTCTCTGAAAACCTCACTGAGCTCGCGTTTGAAMACCAACCTCCCT 278
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QY 2950 TCTCCCGAGGTCATGACAGGATCTGCTCCCTGCTGCTTCCCTTACCAAGTCTGACACCGCT 3009
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Db 277 TCTCCCGAGGTCATGACAGGATCTGCTCCCTGCTGCTTCCCTTACCAAGTCTGACACCGCT 218
| | | | |
QY 3010 GACTCCCGAGGAGTCTTCCCTGAGTCTGACACCTTCTTCTTCTGCTTCAAGTTGGGGCAG 3069
| | | | |
Db 217 AACTCCCGAGGAGTCTTCCCTGAGTCTGACACCTTCTTCTTCTGCTTCAAGTTGGGGAAA 158
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QY 3070 ACTCTGATCCCTTCTGCTCGGAGAAATGGCAGGGTAATCTGAGCCCTTCTTCACTCCTT 3129
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Db 157 ACTCTGATCCCTTCTGCTCGGAGAAATGGCAGGGTAATCTGAGCCCTTCTTCACTCCTT 98
| | | | |
QY 3130 TACCTAGCTGACCCCTTCACTCTCCCTCCCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 3189
| | | | |
Db 97 TACCTAGCTGACCCCTTCACTCTCCCTCCCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 38
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QY 3190 ACTGCTTGTACAGAGACTGTTTATTTTATTT 3220
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Db				
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	BX363741/c			EST 05-MAY-2003
	LOCUS			
	DEFINITION	Homo sapiens B CELLS (RAMOS CELL LINE) COT 25-NORMALIZED		
		Homo sapiens cDNA clone CSODL005YC17 3-PRIME, mRNA sequence.		
	BX363741			
	ACCSSION	BX363741.1	GI:30384744	
	VERSION			
	KEYWORDS			
	SOURCE			
	ORGANISM			
		Homo sapiens (human)		
		Homo sapiens		
		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
		Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
		Li, W.B., Gruber, C., Jessee, J. and Polayes, D.		
		(bases 1 to 1201)		
		Full-length cDNA libraries and normalization		
		Unpublished (2001)		
		Contact: Genoscope		
		Genoscope - Centre National de Sequencage		
		BP 191 91006 EVRY cedex - France		
		Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr		
		Library was constructed by Life Technologies, a division of		
		Invitrogen. This sequence belongs to sequence cluster 907.f For		
		more information about this cluster, see		
		http://www.genoscope.cns.fr/		
		cgi-bin/cluster.cgi?seq=CSODL005AB09NP1&cluster=907.f. Contact :		
		Feng Liang Email : fliang@lifetech.com URL :		
		http://fulllength.invitrogen.com/ InvitroGen Corporation 1600		
		Paradise Avenue Genoscope sequence ID : CSODL005AB09NP1.		
		Location/Qualifiers		
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		25-NORMALIZED"		
		/notes="1st strand cDNA was primed with a NotI-oligo(dT)		
		primer. Five prime end enriched, double-strand cDNA was		
		digested with Not I and cloned into the Not I and EcoR V		
		sites of the pCMVSPORT 6 vector. Library was normalized."		
	FEATURES			
	source			
		Query Match	26.5%; Score 929.4; DB 13; Length 1201;	
		Best Local Similarity	95.5%; Pred. No. 1.6e-219;	
		Matches 1002; Conservative	16; Mismatches 23; Indels 8; Gaps 6;	
	Qy	2157	GAACTGGCAGCATCCCGGGAGATGTGAAGTGCCCGTGTACCAAGGTCAGTGGTGGG	2216
	Db	1042	GATCTGAATGGCAGCATCCCCGGGAGWKGARGTCCCGTGTGCC-RGGTCAGTGGTGGG	984
	Qy	2217	GCCGCCCTGGTCCCGACGAGTCTACTGSCCCACTTTGTCACTGCTACTGCTCTCTTT	2276
	Db	983	--CCGCCCTGGYGCCCGACGAGTCOWAYTG--CCCATTGTCACTGTCACTGCTCTCTTT	928
	Qy	2277	GCCTTAGTGTTCAGAGGCCCTCATCATCTCGTGGCCCTCCCATTTGAGACACTCCGG	2336
	Db	927	GCCTTAGTGTTCAGAGGCCCTCATCATCTCGT-GCCTCCCATTTGAGACACTCCGG	870
	Qy	2337	GCTCGGGCAAGTTCAGGCTGTGAGACCTCGGCCCTGGGGAGAAGGCCCGCTTAAGC	2396
	Db	869	GCTCGGGCAAGTTCAGGCTGTGAGACCTCGGCCCTGGGGAGAAGGCCCGCTTAAGC	810
	Qy	2397	AGAGAGCAACACCTCCAGTCTCCCAAGGATTCAGGACCTCTCCAGTGTATGGACGCT	2456
	Db	809	AGAGAGCAACACCTCCAGTCTCCCAAGGATTCAGGACCTCTCCAGTGTATGGACGCT	750
	Qy	2457	GACAACAACCTGCCTAGGACCTGAGGAGTAACTTAGCACAGCCCGGCTCGCGT	2516

Invitrogen. This sequence belongs to sequence cluster 907.f For more information about this cluster, see

http://www.genoscope.cns.fr/cgi-bin/cluster.cgi?seq=CS0BA10432D06_CS04076_1&cluster=907.f.
Contact : Feng Liang Email : fliang@lifetech.com URL : <http://fulllength.invitrogen.com/> Invitrogen Corporation 1600 Faraday Avenue Genoscope sequence ID : CS0BA10432D06_CS04076_1.

FEATURES

Location/Qualifiers
1..922
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DL005YC17"
/cell_type="RAMOS CELL LINE"
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/note="1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

Query Match 25.0%; Score 876; DB 13; Length 922;
Best Local Similarity 98.8%; Pred. No. 2.7e-206;
Matches 879; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

1471 CCCAGGGCTTGATGGGACAGCATTCTGTCATCTGGTGGAGAGATTGAGTGT 1530
Db CCCAGGCTTGATGGGACAGCATTCTGTCATCTGGTGGAGAGATTGAGTGT 860
QY TCCCAAGGCTGTGTAAGTGGGACAGCAGTGTCTATCTGGTGGAGAGATTGAGTGT 1590
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QY TCCCTGACCTGAACTGTTCCCAACTGTCAGCTGGGCCCCCACCAGGGTGCAGTGT 1650
Db TCCCTGACCTGAACTGTTCCCAACTGTCAGCTGGGCCCCCACCAGGGTGCAGTGT 740
QY TAGGCTTCTCAGAGGCTCTGAGGGTGGCCCCCAGAGCACTGATGCTATGAGAGCT 1710
Db TAGGCTTCTCAGNAGGCTCTGAGGGTGGCCCCCAGAGCACTGATGCTATGAGAGCT 680
QY GTGTGGAGTGTCTTGTCCCGGAGCCCCCACTGTGCTGGGACCTGAGTCCCGAACCT 1770
Db GTGTGGAGTGTCTTGTCCCGGAGCCCCCACTGTGCTGGGACCTGAGTCCCGAACCT 620
QY GTTGCCTCTGTCGCCCACTGAACTCTCTGAGCAGGACATGAGCGGGGAAAC 1830
Db GTTGCCTCTGTCGCCCACTGAACTCTCTGAGCAGGACATGAGCGGGGAAAC 560
QY CAGAGTGGGCATGTGCCAGTGGCCCCCATGAGCAGGAGCTTTCGGCCTCAGAGCGCCGC 1890
Db CAGAGTGGGCATGTGCCAGTGGCCCCCATGAGCAGGAGCTTTCGGCCTCAGAGCGCCGC 500
QY AAATCATTTAAGAAGTCTGCTGCTCCTTAATCTGATCTGAGCTCCCTGCCCCCACC 1950
Db AAATCATTTAAGAAGTCTGCTGCTCCTTAATCTGATCTGAGCTCCCTGCCCCCACC 440
QY TGTGAGCTTGGCCTCTTATTATTGAGTCTATGCCCCCAGCAGTCCCGAGAGCTCTTT 2010
Db TGTGAGCTTGGCCTCTTATTATTGAGTCTATGCCCCCAGCAGTCCCGAGAGCTCTTT 380
QY CACTGTGTCAATGGCTCCCTCTTGTGATGATGTCAGGATGAGATTGGGGGTCTTACC 2070
Db CCACTGTGTCAATGGCTCCCTCTTGTGATGATGTCAGGATGAGATTGGGGGTCTTACC 320
QY AGTGTGGGCACTGAGATGCTTTTATACCTCTGATCTCTCTACTGGGTGACAGCC 2130
Db AGTGTGGGCACTGAGATGCTTTTATACCTCTGATCTCTCTACTGGGTGACAGCC 260
QY AGGACAGACCTGGCCTTGATCTGAGAGGATCCCGGAGGATCCCGGAGGATGTGAAG 2190

Db 259 AGGACAGACCTGGCCTTGATCTGAACCTGGCAGGATCCCGGAGGATGTGAAGG 200
QY TCCGTTTACCAGAGCTAGTGGTGGGCGGCCCTGGTGGCCAGCAGTCTTACTGGGCCC 2250
Db TCCGTTTACCAGAGCTAGTGGTGGGCGGCCCTGGTGGCCAGCAGTCTTACTGGGCCC 140
QY ACTTGTGTCACGTGTCACGTGCTCTTTGGCTTAGTGTCTTTCAGGAGCCCTCATCTCTCG 2310
Db ACTTGTGTCACGTGTCACGTGCTCTTTGGCTTAGTGTCTTTCAGGAGCCCTCATCTCTCG 80
QY TGGCCTTCCCATTTGAGAGCACTCCGGGCTCGGGCAAGGTTTCAGGGCTGT 2360
Db TGGCCTTCCCATTTGAGAGCACTCCGGGCTCGGGCAAGGTTTCAGGGCTGT 30

RESULT 9

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

CONTACT

Genoscope - Centre National de Sequencage

Bp 191 91006 EVRY cedex - France

Email: segref@genoscope.cns.fr; Web: www.genoscope.cns.fr

Library was constructed by Life Technologies, a division of

Invitrogen. This sequence belongs to sequence cluster 907.f For

more information about this cluster, see

http://www.genoscope.cns.fr/cgi-bin/cluster.cgi?seq=CS0BAG0532H06_C

S05040_1&cluster=907.f. Contact : Feng Liang Email :

fliang@lifetech.com URL : <http://fulllength.invitrogen.com/>

Invitrogen Corporation 1600 Faraday Avenue Genoscope sequence ID :

CS0BAG0532H06_CS05040_1.

Location/Qualifiers

1..926

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

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/note="1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."

Query Match 24.4%; Score 856.6; DB 13; Length 926;
Best Local Similarity 98.1%; Pred. No. 1.8e-201;
Matches 909; Conservative 0; Mismatches 14; Indels 4; Gaps 4;

QY TGGCAGCCATCCCTTCGACCCAGGTCGTCTCTTCTTCGAGG-ACACAGCCAGCGAG 962
Db TGGCAGCCATCCCTTCGACCCAGGTCGTCTCTTCTTCGAGGAGACAGCCAGCGAG 60
QY TTTGACTTCTTTGAGAGGCTCCACATCGCGGGTGGCTAGAGTGTGAAGATGACGTG 1022
Db TTTGACTTCTTTGAGAGGCTCCACATCGCGGGTGGCTAGAGTGTGAAGATGACGTG 120
QY GCGGGCGAAAGCTGCTGAGAGAGTGGACACCTTCCTGAGAGCCAGCTGCTGTC 1082

Db	121	GGGGGGAAAGCTGCTGCGAGAAAGTGGACCACTTCTCTGAAGGCCCGAGCTGCTCTGC	180
Qy	1083	ACCAGCGGGGAGCTGCCCTTCAACGTCATCGCCACCGGTCCTGCTCCCGCCGAT	1142
Db	181	ACCAGCGGGGAGCTGCCCTTCAACGTCATCGCCACCGGTCCTGCTCCCGCCGAT	240
Qy	1143	TCTCCCAAGCTCCCAACATCTACGAGTCTTACCTCCCACTCCCACTGGCAGGTTGGGGGACC	1202
Db	241	TCTCCCAAGCTCCCAACATCTACGAGTCTTACCTCCCACTGGCAGGTTGGGGGACC	300
Qy	1203	AGGAGCTCGGGTTGTGCTTCTCTCTTGGACATTGAACGTGTCTTTTAAGGGGAAA	1262
Db	301	AGGAGCTCTGGGTTGTGCTTCTCTCTTGGACATTGAACGTGTCTTTTAAGGGGAAA	360
Qy	1263	TACAAAGAGTTGAACAAAGAAACTTCACGTGGACTACTTATATAGGGCCCTTGAGACCAAC	1322
Db	361	TACAAAGAGTTGAACAAAGAAACTTCACGTGGACTACTTATAGGGCCCTTGAGACCAAC	420
Qy	1323	CCCGGCGAGGACGTTGCTAGTGGGCCCCCTCTCTGATAAGGCCCTTGACCTTCATGAAG	1382
Db	421	CCCGGCGAGGACGTTGCTAGTGGGCCCCCTCTCTGATAAGGCCCTTGACCTTCATGAAG	480
Qy	1383	GACCATTTCGTGATGAGTAGACAAGTGGTGGGCGACGCCCTGCTGTGTGAATCTGGCGGTG	1442
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Qy	1443	GAGTATACACGGCTTGACGTGGAGACAGCCACAGGCGCTTGATAGGGCAAGCCATCTTTGTC	1502
Db	541	GAGTATACACGGCTTGACGTGGAGACAGCCACAGGCGCTTGATAGGGCAAGCCATCTTTGTC	600
Qy	1503	ATGTACCTGGGAACCAACACAGGTCGCTCCACAGGCTGTGGTAACTGGGGACAGCAGT	1562
Db	601	ATGTACCTGGGAACCAACACAGGTCGCTCCACAGGCTGTGGTAACTGGGGACAGCAGT	660
Qy	1563	GCTCATCTGGTGGAGAGATTACAGTGTTCCTGACCTGAACTGTTCGCAACTCTGACG	1622
Db	661	GCTCATCTGGTGGAGAGATTACAGTGTTCCTGACCTGAACTGTTCGCAACTCTGACG	720
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Db	721	CTGGCCCCCAACCCAGGGTGCAAGTGTGTTGTAGGCTTCTCAGAGAGGTGTCTGGNAGGGTGC	780
Qy	1681	CCCGAGCCAACTGTAGTCTCTATAGAGACTGTGTGGACTGTCTCTGCCCGGACACCCC	1740
Db	781	CCCGAGCCAACTGTAGTCTCTATAGAGACTGTGTGGACTGTCTCTGCCCGGACACCCC	840
Qy	1741	ACTGTGCTGGGACCCCTGAGTCCCGAAACGTGTGCTCTCTGCTGCTCCGCCCAACTGAACT	1800
Db	841	-CTGTGCTGGGACCCCTGAGTCCCGAACCTGTGTGCTTCTGTCTGCCCCCAACTTGACT	899
Qy	1801	CCTGGAAGCAGGACATGAGCGGGGA	1827
Db	900	CCTTGGAAAGCACATGAGCGGGGAA	926

[illegible]

BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr Web : www.genoscope.cns.fr
The seqref@genoscope.cns.fr Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 907.f. For more information about this cluster, see
<http://www.genoscope.cns.fr/cgi-bin/cluster.cgi?seq=CS0DL005A9Q1&cluster=907.f>. Contact : Feng Liang Email: liang@lifetech.com URL : <http://fulllength.invitrogen.com/> Invitrogen sequence ID : CS0DL005A909p1
Paradise Avenue Invitrogen

FEATURES

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/clone="CS0DL005VC17"
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25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo (dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."

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ORIGIN

Query Match	24.2%	Score 849.2	DB 13	Length 1201
Best Local Similarity	97.0%	Pred. No. 1.5e-199		
Matches 871; Conservative 4; Mismatches 22; Indels 1; Gaps 1				
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Qy	258	TTCCAACTGCTTGAGCTGCTGTGCCAGACGACGACCGCGGGGGGAGGGGGGAGGGGGCC	317	
Db	128	TTCCAACTGCTTGAGCTGCTGTGCCAGACGACGACCGCGGGGGGAGGGGGGAGGGGGCC	187	
Qy	318	ATGCCCAGGGTCAGATACTATGACAGGGATGAAAGTAGGGCACATTAGTCTTCTTCACCCAG	377	
Db	188	ATGCCCAGGGTCAGATACTATGACAGGGATGAAAGTAGGGCACATTAGTCTTCTTCACCCAG	247	
Qy	378	AAGGGCTCCAGGATTTTGACACTCTGCTCTGAGTGGTGATGAAATACCTCTACCGTG	437	
Db	248	AAGGGCTCCAGGATTTTGACACTCTGCTCTGAGTGGTGATGAAATACCTCTCTACCGTG	307	
Qy	438	GGGSCTCGAGAAGCCATTCTGGCCCTTGATATCCAGGATCCAGGGGTCCCCAGGCTAAAG	497	
Db	308	GGGSCTCGAGAAGCCATTCTGGCCCTTGATATCCAGGATCCAGGGGTCCCCAGGCTAAAG	367	
Qy	498	AACATGATACCGTGGCCAGCCAGTGACAGAAAAAGAGTGAATGTCTTTAAGAAGAAG	557	
Db	368	AACATGATACCGTGGCCAGCCAGTGACAGAAAAAGAGTGAATGTCTTTAAGAAGAAG	427	
Qy	558	AGCAATGAGACACAGTGTTCACCTTCATCCGTCTCGTGTTCCTTACAAGTGACCCAT	617	
Db	428	AGCAATGAGACACAGTGTTCACCTTCATCCGTGTCTCTGGTTCCTTACAAGTGACCCAT	487	
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Db	488	CTCTACACCTCGGCGACCTTCGCGCTTCAGCCCTGTCTGTACCTTCATTGAACCTCAAGAT	547	
Qy	678	TCTTACCTGTGGCCCATCTCGAGGACAAGGTTCATGGAGGGAAGGCGCAAGCCCTTT	737	
Db	548	TCTTACCTGTGGCCCATCTCGAGGACAAGGTTCATGGAGGGAAGGCGCAAGCCCTTT	607	
Qy	738	GACCCCGCTCAACAGCATACGGCTGTCTTGTTGATGGATGGCTCTATTCTTGGTACTATG	797	
Db	608	GACCCCGCTCAACAGCATACGGCTGTCTTGTTGATGGATGGCTCTATTCTTGGTACTATG	667	
Qy	798	AACAACTTCCTGGGCAAGTGAGCCCATCTCTGATGCGCAACATGGGATCCAGAGCTGTCTC	857	
Db	668	AACAACTTCCTGGGCAAGTGAGCCCATCTCTGATGCGCAACATGGGATCCAGAGCTGTCTC	727	

QY 858 AAGACGCAAACTTCTCCGCTGGCTGCTCATATGAGCGCTCTTTTGTGGCAGCCATCCCT 917
 DB 728 AAGACGCAAACTTCTCCGCTGGCTGCTCATATGAGCGCTCTTTTGTGGCAGCCATCCCT 787
 QY 918 TCGACCCAGGTGCTGCTACTTCTTCTCGAGGAGACAGCCAGGAGTTTGACTTCTTTGAG 977
 DB 788 TCGACCCAGGTGCTGCTACTTCTTCTCGAGGAGACAGCCAGGAGTTTGACTTCTTTGAG 847
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 DB 848 AGCTCCACATCGGGTGGCTAGAGTCTCGAAGATGAGTGGGGGGG-AAAATG 906
 QY 1038 CTCGAGAGAGTGGACCACTTCTCGAAGGCCAGCTGCTGCAACCCAGCGGGGC 1095
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 5' mRNA sequence.

ACCESSION BQ057192
 VERSION BQ057192.1 GI:19816532
 KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM

Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

AUTHORS NIH-MGC <http://mgi.nci.nih.gov/>.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgabs@mail.nih.gov

Tissue Procurement: Lou Staudt

cDNA Library Preparation: Rubin Laboratory

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

Plate: L1CM2062 row: 1 column: 16

High quality sequence stop: 714.

FEATURES

source

1..974

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/clone="IMAGE:5812383"

/tissue_type="lymphoma, cell line"

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/clone_lib="NIH_MGC_99"

/note="Organ: lymph; Vector: pOTB7; Site 1: XhoI; Site 2:

EcoRI; cDNA made by oligo-dT priming. Directionally cloned

into EcoRI/XhoI sites using the following 5' adaptor:

GCACAG(G). Size-selected >500bp for average insert size

1.8kb. Library constructed by Ling Hong in the laboratory

of Gerald M. Rubin (University of California, Berkeley)

using ZAP-cDNA synthesis kit (Stratagene) and Superscript

II RT (Life Technologies). Note: this is a NIH_MGC

Library."

ORIGIN

Query Match 23.6%; Score 827.4; DB 13; Length 974;
 Best Local Similarity 92.6%; Pred. No. 3.4e-194;
 Matches 902; Conservative 0; Mismatches 67; Indels 5; Gaps 3;

QY 191 TCTGTGGCTGAGCATGGCCCTCCAGCCCTGGGCTGAGCCCTGGAGCCTCTCTGGGCCT 250
 DB 1 TCTGTGGCTGAGCATGGCCCTCCAGCCCTGGGCTGAGCCCTGGAGCCTCTCTGGGCCT 60

RESULT 12
 BX390196

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

BX390196 960 bp mRNA linear EST 08-MAY-2003
 BX390196 Homo sapiens NEUROBLASTOMA COT 50-NORMALIZED Homo sapiens
 cDNA clone CSDD003YE08 5-PRIME, mRNA sequence.

BX390196

BX390196.1 GI:30463276

EST.

QY 251 TTTCTCTTCCAACTGCTTTCAGCTGCTGCTGCGAGCAGCCGCGGGGGAGCGCGGCA 310
 DB 61 TTTCTCTTCCAACTGCTTTCAGCTGCTGCTGCGAGCAGCCGCGGGGGAGCGCGGCA 120
 QY 311 GGGGCCCATCCCGAGGGTCAGATACATATGAGGGGATGAACGTAGGGCACTTAGCTTCTT 370
 DB 121 GGGGCCCATCCCGAGGGTCAGATACATATGAGGGGATGAACGTAGGGCACTTAGCTTCTT 180
 QY 371 CCACCAAGAGGGGCTCCAGGATTTTGCACACTCTGCTCCCTGAGTGGTATGGAATACTCT 430
 DB 181 CCACCAAGAGGGGCTCCAGGATTTTGCACACTCTGCTCCCTGAGTGGTATGGAATACTCT 240
 QY 431 CTACGTGGGGGCTCGAGAGCCATTCTGGCTTGGATATCCAGGATCCAGGGGTCCCCAG 490
 DB 241 CTACGTGGGGGCTCGAGAGCCATTCTGGCTTGGATATCCAGGATCCAGGGGTCCCCAG 300
 QY 491 GCTAAAGAAATGATATCCGTGGCCAGCCAGTGCAGAAAAAGAGTGAATGTGCCTTTAA 550
 DB 301 GCTAAAGAAATGATATCCGTGGCCAGCCAGTGCAGAAAAAGAGTGAATGTGCCTTTAA 360
 QY 551 GAAGAGAGCAATGAGACACAGTGTTCCTCACTCCCTGCTGCTGCTTCTTACATGT 610
 DB 361 GAAGAGAGCAATGAGACACAGTGTTCCTCACTCCCTGCTGCTGCTTCTTACATGT 420
 QY 611 CACCCATCTCTACACCTGCGGCACCTTCGCTTCAGCCCTGCTTGTACCTTTCATTGAAC 670
 DB 421 CACCCATCTCTACACCTGCGGCACCTTCGCTTCAGCCCTGCTTGTACCTTTCATTGAAC 480
 QY 671 TCAAGATTCCTACCTGTTGCCATCTCGAGGACAAGTCAATGAGGAGAAAGCCCAAG 730
 DB 481 TCAAGATTCCTACCTGTTGCCATCTCGAGGACAAGTCAATGAGGAGAAAGCCCAAG 540
 QY 731 CCCCTTTGACCCCGCTCACAAGCATACGGCTGCTTGGTGGATGGGATGCTCTATTCTGG 790
 DB 541 CCCCTTTGACCCCGCTCACAAGCATACGGCTGCTTGGTGGATGGGATGCTCTATTCTGG 600
 QY 791 TACTATGAACAACCTTCTGCGCAGTGCATCTGATGCGCACACTGGGATCCCAAGCC 850
 DB 601 TACTATGAACAACCTTCTGCGCAGTGCATCTGATGCGCACACTGGGATCCCAAGCC 660
 QY 851 TGTCTCAAGACCGCAACCTTCTCCGCTGCTGCATCATGAGCCCTCTTTTGGGAGC 910
 DB 661 TGTCTCAAGACCGCAACCTTCTCCGCTGCTGCATCATGAGCCCTCTTTTGGGAGC 720
 QY 911 CATCCCTTCGACCCAGGTGCTTACTTCTTCTTGGAGGACAGCCAGCGATTTGACTT 970
 DB 721 CATCCCTTCGACCCAGGTGCTTACTTCTTCTTGGAGGACAGCCAGCGATTTGACTT 780
 QY 971 CTTTGAGAGGCTCCACACATCGCGGTGG-CTAGAGTCTCAAGATGAGTGGGC-GGC 1028
 DB 781 CTTTGAGAGGCTCCACACATCGCGGTGGCTTCTTCTTGGAGGACAGCCAGCGATTTGACTT 840
 QY 1029 GAAAGAGTGTGCGAGAGAA---GTGGACCACTTCTTCTGAGGCGCCAGCTGCTCTGCACC 1085
 DB 841 GAAAGAGTGTGCGAGAGAAAGTGGACCCCTTCTTCTTGAAGCCCAAGCTCTCTGGCCC 900
 QY 1086 CAGCCGGGGAGTGGCCCTTCAAGTATCCGCGACAGCGGTCTCTCTCCCGCGGATCT 1145
 DB 901 CCAGCCGGGGAGTGGCCCTTTCACGTCAATCCCGCCCGGGGCTCTGGCTCCGCC 960
 QY 1146 CCACAGCTCCCCA 1159
 DB 961 CCGAATTTTCCCCA 974

/notes="Organ: placenta; Vector: pT73D (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was primed with a Not I - oligo (dT) primer [5', AACTGGAAGATTTCGGCGCCGACGAAATTTTCTTTTCTTTT 3'], double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT73 vector. Library went through one round of normalization. Library constructed by Bento Soares and M.Fatima Bonaldo. "

ORIGIN	Query Match	22.1%;	Score 775;	DB 13;	Length 801;
	Best Local Similarity	99.4%;	Pred. No. 3.4e-181;		
	Matches	797;	Conservative	0;	Mismatches 3; Indels 2; Gaps 2;
QY	2185	TGAAGTCCCGTTACACAGGGTCAGTGGTGGGGCCGCTGGTGGCCAGCAGTCTCTACT	2244		
DB	1	TGAAGGTCGCGTGAACC-GGGTCAGTGGTGGGGCCGCTGGTGGCCAGCAGTCTCTACT	59		
QY	2245	GGCCCCCACTTTGTCACTGTCTCACTGTCTCTTTTGGCTTTAGTGTCTTTTTCAGGAGCCCTCATCA	2304		
DB	60	GGCCCCCACTTTGTCACTGTCTCACTGTCTCTTTTGGCTTTAGTGTCTTTTTCAGGAGCCCTCATCA	119		
QY	2305	TCCTGTGGCTCCCATTTAGAGACACTCGGGCTCGGGCAGAGTTTCAGGCTGTGAGA	2364		
DB	120	TCCTGTGGCTCCCATTTAGAGACACTCGGGCTCGGGCAGAGTTTCAGGCTGTGAGA	179		
QY	2365	CCCTGGCCCTGGGGAGAGGCCCGCTTAAGCAGAGAGCAACCTCCAGTCTCCCAAGG	2424		
DB	180	CCCTGGCCCTGGGGAGAGGCCCGCTTAAGCAGAGAGCAACCTCCAGTCTCCCAAGG	239		
QY	2425	AATGAGACCTCTGCGCAGTGTATGTGACGTGTGACCAACCACTGCTAGGCACTGAGGTAG	2484		
DB	240	AATGAGACCTCTGCGCAGTGTATGTGACGTGTGACCAACCACTGCTAGGCACTGAGGTAG	239		
QY	2485	CTTAAACTCTAGGCACAGCGCGGCTGGGTGAGGACCTGGCCCATGTGCTGGCG	2544		
DB	300	CTTAAACTCTAGGCACAGCGCGGCTGGGTGAGGACCTGGCCCATGTGCTGGCG	359		
QY	2545	GCCCAAGCAGCCCTGACTAGGATGACAGCAGCACAACCAACCACTTTCTCCCTGAG	2604		
DB	360	GCCCAAGCAGCCCTGACTAGGATGACAGCAGCACAACCAACCACTTTCTCCCTGAG	419		
QY	2605	AGGAGCTTCTCTACTCTGATCATCTGATGACACTCAGCAGGCTGATGACAGCAGTCTG	2664		
DB	420	AGGAGCTTCTCTACTCTGATCATCTGATGACACTCAGCAGGCTGATGACAGCAGTCTG	479		
QY	2665	CCTCCCTATGGACTCCCTTCTTCAAGACATGAGTCTTCAACAGGTTGGGGCTAC	2724		
DB	480	CCTCCCTATGGACTCCCTTCTTCAAGACATGAGTCTTCAACAGGTTGGGGCTAC	539		
QY	2725	CCCCAGACCTCTCTACACTGATTTGAAGACCTGGAGAGGATCTTCAAGTTCTGGCC	2784		
DB	540	CCCCAGACCTCTCTACACTGATTTGAAGACCTGGAGAGGATCTTCAAGTTCTGGCC	599		
QY	2785	ATTCCAGGAGCCCTCCAGAAACACAGTGTTTTCAAGAGACCCCTTAAACACCTGTGCCC	2844		
DB	600	ATTCCAGGAGCCCTCCAGAAACACAGTGTTTTCAAGAGACCCCTTAAACACCTGTGCCC	659		
QY	2845	AGGACCTATGTTAATGACCAACCAACATCTTAAACATCATATGCTAATGACCACTCT	2904		
DB	660	AGGACCTATGTTAATGACCAACCAACATCTTAAACATCATATGCTAATGACCACTCT	719		
QY	2905	GGAAACTCCACTTGAAGCTCGCGCTTTGGACACCAACCACTCCCTTCTCCAGGGTCATG	2964		
DB	720	GGAAACTCCACTTGAAGCTCGCGCTTTGGACACCAACCACTCCCTTCTCCAGGGTCATG	779		
QY	2965	CA-GGGATCTGCTCCCTCTGC	2985		
DB	780	CAGGGGATCTGCTCCCTCTGC	801		

RESULT 14

CB243787/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
PUBMED
COMMENT

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797 bp mRNA linear EST 12-FEB-2003
UI-CF-FNO-agg-a-05-0-UI.s1 UI-CF-FNO Homo sapiens cDNA clone
UI-CF-FNO-agg-a-05-0-UI 3', mRNA sequence.
CB243787
CB243787.1 GI:28365431
EST.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
discovery
Genome Res. 6 (9), 791-806 (1996)
97044477
889548
Contact: McCray, PB
McCray Lab
University of Iowa
2024 University of Iowa Med Labs, Iowa City, IA 52242, USA
Tel: 319 356 4866
Fax: 319 356 7171
Email: paul-mccray@uiowa.edu
Tissue Procurement: Dr. M. J. Welsh, University of Iowa
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Researchers may obtain clones from Research
Genetics (www.reagen.com) or from Open Biosystems
(www.openbiosystems.com).
The following repetitive elements were found in this cDNA
sequence: 1-46, >AT richLow_complexity (matched complement)
Seq primer: M13 FORWARD
POLYA=Yes.
Location/Qualifiers
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-CF-FNO-agg-a-05-0-UI"
/tissue_type="Human Lung Epithelial cells"
/lab_host="DH10B (Life Technologies) (T1 phage resistant)"
/clone_lib="UI-CF-FNO"
/note="Organ: Lung; Vector: pT73-Pac (Pharmacia) with a
modified polylinker; Site 1: EcoR I; Site 2: Not I;
UI-CF-FNO is a subtracted cDNA library derived from two
normalized Human lung epithelial cell libraries (EN1 and
DU1) The library was subtracted according to according to
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. For additional information, contact:
bento-soares@uiowa.edu
TAG TISSUE=Human Lung Epithelial Cell Lines untreated LPS
Ghr to LPS 24h
TAG LIB=UI-CF-FNO
TAG_SEQ=CTGCTCAGGT"

ORIGIN

Query Match 22.0%; Score 772.2; DB 14; Length 797;
Best Local Similarity 99.2%; Pred. No. 1.7e-180;
Matches 774; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
QY 2457 GACACAACTGCTAGGCACTGAGTGTAGCTTAACTTAGGCACAGCCGGGCTGCGGT 2516
DB 797 GACACAACTGCTAGGCACTGAGTGTAGCTTAACTTAGGCACAGCCGGGCTGCGGT 738
QY 2517 GCAGCACCCTGCCATGCTGGCTGGCGGCCCAACAGCCCTACTAGGATGACAGA 2576
DB 737 GCAGCACCCTGCCATGCTGGCTGGCGGCCCAACAGCCCTACTAGGATGACAGA 678
QY 2577 GCACAAAGACACCTCTTCCCTTGAGAGGAGCTTCTGCTACTCTGCTACTGATGAC 2636

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Db      677 GCACAAAAGACCACCTTTCTCCCTGAGAGAGAGCTTCTGCTACTCTGATCAGTATGAC 618
QY      2637 ACTCAGAGGGTGTATGACAGAGTCTCCCTCCCTATGAGAGTCCCTTCTTACCAAGCAC 2696
Db      617 ACTCAGAGGGTGTATGACAGAGTCTCCCTCCCTATGAGAGTCCCTTCTTACCAAGCAC 558
QY      2697 ATGAGCTCTTAACAGAGGTGGGGTACCCAGAGAGTCTCCCTTACAGTATGATTAAGA 2756
Db      557 ATGAGCTCTTAACAGAGGTGGGGTACCCAGAGAGTCTCCCTTACAGTATGATTAAGA 498
QY      2757 ACTCGAGAGAGTCTTCACTGCTGGCCATTCAGAGAGTCTCCAGAGAGTCTCCAGAGAGTCTTTC 2816
Db      497 ACTCGAGAGAGTCTTCACTGCTGGCCATTCAGAGAGTCTCCAGAGAGTCTCCAGAGAGTCTTTC 438
QY      2817 AAGAGACCTTAAACACCTCTGCTCCAGAGAGTCTTGAATGAACACACACACACTTA 2876
Db      437 AAGAGACCTTAAACACCTCTGCTCCAGAGAGTCTTGAATGAACACACACACACTTA 378
QY      2877 AACATCATATGCTTAACATGACCTCTGAGAGTCTTGAATGAACACACACACACTTA 2936
Db      377 AACATCATATGCTTAACATGACCTCTGAGAGTCTTGAATGAACACACACACACTTA 318
QY      2937 ACCACACTCTTCCAGAGTCTGCTCCAGAGAGTCTTGAATGAACACACACACACTTA 2996
Db      317 ACCACACTCTTCCAGAGTCTGCTCCAGAGAGTCTTGAATGAACACACACACACTTA 258
QY      2997 GTCTGTCACCGTCTGCTCCAGAGAGTCTTGAATGAACACACACACACTTA 3056
Db      257 GTCTGTCACCGTCTGCTCCAGAGAGTCTTGAATGAACACACACACACTTA 198
QY      3057 TCAGTTGGGGAGAGTCTGATCCCTTCTGAGAGTCTTGAATGAACACACACACACTTA 3116
Db      197 TCAGTTGGGGAGAGTCTGATCCCTTCTGAGAGTCTTGAATGAACACACACACACTTA 138
QY      3117 TTCTTCACTCTTACCTAGTCTGAGAGTCTTGAATGAACACACACACACTTA 3176
Db      137 TTCTTCACTCTTACCTAGTCTGAGAGTCTTGAATGAACACACACACACTTA 78
QY      3177 TGGGATTCAGAAACTCTGTCAGAGTCTTGAATGAACACACACACACTTA 3236
Db      77 TGGGATTCAGAAACTCTGTCAGAGTCTTGAATGAACACACACACACTTA 18

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RESULT 15
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LOCUS   BQ883972
DEFINITION AGENCOURT_8616305 NIH_MGC_113 Homo sapiens cdna clone IMAGE:6302388
5', mRNA sequence.
ACCESSION BQ883972
VERSION   BQ883972.1
KEYWORDS  EST.
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens
REFERENCE 1 (bases 1 to 912)
AUTHORS   NIH-MGC http://mgi.mcg.gov/
TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL   Unpublished (1999)
COMMENT   Contact: Robert Strausberg, Ph.D.
          Email: cgaabs@mail.nih.gov
          Tissue Procurement: Dr. Mark Watson
          cDNA Library Preparation: Rubin Laboratory
          DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
          Clone distribution: Agencourt Bioscience Corporation
          found through the I.M.A.G.E. Consortium/LLNL at:
          http://image.llnl.gov
          Plate: LLCM2519 row: m column: 13
          High quality sequence stop: 601.
          Location/Qualifiers
            1. .912
              /organism="Homo sapiens"

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/mol_type="mrna"
/db_xref="taxon:9606"
/clone="IMAGE:6302388"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_113"
/notes="Organ: spleen; Vector: pOTB7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH_MGC Library."

```

ORIGIN

```

Query Match      21.9%; Score 768.2; DB 13; Length 912;
Best Local Similarity 96.5%; Pred. No. 1.8e-179; Indels 7; Gaps 5;
Matches 839; Conservative 0; Mismatches 23;

QY      1414 GGACGCCCTGCTGGTGAATCTGGGTGGAGTATACAGGCTTGCAGTGGAGACAGCC 1473
Db      1      GGACGCCCTGCTGGTGAATCTGGGTGGAG-ATACACGGCTTGCAGTGGAGACAGCC 59

QY      1474 AGGGCCTTATGGGACAGCCATCTGTCTATCTGCTGGACACACAGGTCGCTCC 1533
Db      60      AGGGCCTTATGGGACAGCCATCTGTCTATCTGCTGGACACACAGGTCGCTCC 119

QY      1534 ACAAGGCTGTGTAGTGGGACAGCAGTGTCTATCTGCTGGAGAGATTCAGCTGTTC 1593
Db      120      ACAAGGCTGTGTAGTGGGACAGCAGTGTCTATCTGCTGGAGAGATTCAGCTGTTC 179

QY      1594 CTGACCTGAACTGTTCGAACTTGCAGTGTGGGACCACTGCTGGAGTGTGTGTAG 1653
Db      180      CTGACCTGAACTGTTCGAACTTGCAGTGTGGGACCACTGCTGGAGTGTGTGTAG 239

QY      1654 GCTTCTCAGAGGTGTCTGGAGGTGCTGGAGGTGCTGGAGGTGCTGGAGGTGCTG 1713
Db      240      GCTTCTCAGAGGTGTCTGGAGGTGCTGGAGGTGCTGGAGGTGCTGGAGGTGCTG 299

QY      1714 TGAGTGTGTCTTGGCCGGGACCCCTGCTGCTGGAGTGTGGAGTGTGGAGTGTGG 1773
Db      300      TGAGTGTGTCTTGGCCGGGACCCCTGCTGCTGGAGTGTGGAGTGTGGAGTGTGG 359

QY      1774 GCCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1833
Db      360      GCCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 419

QY      1834 AGTGGGATGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1893
Db      420      AGTGGGATGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 479

QY      1894 TCATTAAGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1953
Db      480      TCATTAAGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 539

QY      1954 CAGCCTTGGCTCTTATTATTGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2013
Db      540      CAGCCTTGGCTCTTATTATTGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 599

QY      2014 CTGCTTACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2073
Db      600      CTGCTTACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 659

QY      2074 GCTGGGCACTGAGAAATGGCTTTTTCATACCTGCTGCTGCTGCTGCTGCTGCTG 2133
Db      660      GCTGGGCACTGAGAAATGGCTTTTTCATACCTGCTGCTGCTGCTGCTGCTGCTG 719

QY      2134 ACCAGACCTT-GGCTTGGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2191
Db      720      AACAGACCTTGGGCTTGGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 779

QY      2192 CCGTTTGACCAAGGTTCAGTGG--TGGGGCGGCTGCTGCTGCTGCTGCTGCTGCTG 2249

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Db 780 CCCCTTGACCAAGGTCCATGGGTGGGGCCGGCCTGGCTTGCCCAACAATCCTACTGGCCC 839

Qy 2250 C--ACTTGTCACTGTCACTGTCTCTTT 2276

Db 840 CCACTTGGCCACTGTACTGGCCCCCTT 868

Search completed: April 26, 2004, 01:59:12
Job time : 6369.53 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 25, 2004, 07:43:48 ; Search time 1024.65 Seconds
(without alignments)
15422.560 Million cell updates/sec

Title: US-10-051-835-13
Perfect score: 3505
Sequence: 1 ggcttgcatgatggcac.....tttgggccaaccacaggttg 3505

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 2307579 seqs, 2254313464 residues

Total number of hits satisfying chosen parameters: 5815158

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:
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19: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3505	100.0	3505	15	US-10-051-835-13
2	3060.8	87.3	3143	10	US-09-946-374-276
3	3060.8	87.3	3143	12	US-10-015-395A-276
4	3060.8	87.3	3143	13	US-10-006-485A-276
5	3060.8	87.3	3143	13	US-10-013-907A-276
6	3060.8	87.3	3143	13	US-10-015-499A-276
7	3060.8	87.3	3143	13	US-10-226-254A-276
8	3060.8	87.3	3143	15	US-10-006-856A-276
9	3060.8	87.3	3143	15	US-10-006-818A-276
10	3060.8	87.3	3143	15	US-10-015-393A-276
11	3060.8	87.3	3143	15	US-10-015-869A-276
12	3060.8	87.3	3143	15	US-10-012-121A-276
13	3060.8	87.3	3143	15	US-10-006-116A-276
14	3060.8	87.3	3143	15	US-10-006-117A-276

15	3060.8	87.3	3143	15	US-10-017-527A-276
16	3060.8	87.3	3143	15	US-10-013-913A-276
17	3060.8	87.3	3143	15	US-10-007-194A-276
18	3060.8	87.3	3143	15	US-10-013-430A-276
19	3060.8	87.3	3143	15	US-10-011-671A-276
20	3060.8	87.3	3143	15	US-10-012-755A-276
21	3060.8	87.3	3143	15	US-10-015-386A-276
22	3060.8	87.3	3143	15	US-10-011-692A-276
23	3060.8	87.3	3143	15	US-10-006-768A-276
24	3060.8	87.3	3143	15	US-10-017-610A-276
25	3060.8	87.3	3143	15	US-10-006-063A-276
26	3060.8	87.3	3143	15	US-10-020-063A-276
27	3060.8	87.3	3143	15	US-10-015-391A-276
28	3060.8	87.3	3143	15	US-10-017-407A-276
29	3060.8	87.3	3143	15	US-10-011-833A-276
30	3060.8	87.3	3143	15	US-10-006-041A-276
31	3060.8	87.3	3143	15	US-10-015-822A-276
32	3060.8	87.3	3143	15	US-10-015-387A-276
33	3060.8	87.3	3143	15	US-10-006-130A-276
34	3060.8	87.3	3143	15	US-10-006-172A-276
35	3060.8	87.3	3143	15	US-10-017-253A-276
36	3060.8	87.3	3143	15	US-10-015-392A-276
37	3060.8	87.3	3143	15	US-10-017-306A-276
38	3060.8	87.3	3143	15	US-10-017-867A-276
39	3060.8	87.3	3143	15	US-10-012-064A-276
40	3060.8	87.3	3143	15	US-10-013-909A-276
41	3060.8	87.3	3143	15	US-10-015-671A-276
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ALIGNMENTS

RESULT 1
US-10-051-835-13
; Sequence 13, Application US/10051835
; Publication No. US20030165864A1
; GENERAL INFORMATION:
; APPLICANT: Jones, David A.
; APPLICANT: Jasek, Amy W.
; TITLE OF INVENTION: GENES REGULATED BY DNA METHYLATION IN TUMOR CELLS
; FILE REFERENCE: PA-0044 US
; CURRENT APPLICATION NUMBER: US/10/051,835
; CURRENT FILING DATE: 2002-01-16
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PERL Program
; SEQ ID NO 13
; LENGTH: 3505
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20030165864A1 236992.2
US-10-051-835-13

Query Match	100.0%	Score 3505;	DB 15;	Length 3505;
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			Indels	0;
			Gaps	0;
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Db	1	GGCTTGGCATATGGGACCTTGGAGGCGCGACCTCCCGTCCAGCCAGCTGAGCCTTC	60	
Qy	61	TGTCCCTCCCTCTGGGGCTTGGGAACCCCTTCTTTCTCTCTGAATGSCACCCCG	120	
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Qy	121	CCTAGATCCAGACCCGAGTTCCACTGTGGCTGGTTCAGGGTATGTAGAGCTCC	180	
Db	121	CCTAGATCCAGACCCGAGTTCCACTGTGGCTGGTTCAGGGTATGTAGAGCTCC	180	

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QY 2461 ACAACTGCTAGGCACTGAGGTAGCTTAACTCTAGGACAGGCGCGGCTCCGGTGCAG 2520
Db 2461 ACAACTGCTAGGCACTGAGGTAGCTTAACTCTAGGACAGGCGCGGCTCCGGTGCAG 2520
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Db 2641 AGCAGGATGATGACAGCAGTCTGCTCCCTATGGGACTCCCTTCTACCAAGCACATGA 2700
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RESULT 2

US-09-946-374-276
; Sequence 276, Application US/09946374
; Publication No. US20030073129A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2830P1C1
; CURRENT APPLICATION NUMBER: US/09/946,374
; PRIOR FILING DATE: 2001-09-04
; PRIOR APPLICATION NUMBER: 60/098716
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098723
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098749
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 ; PRIOR APPLICATION NUMBER: 60/105807

Query Match 87.3%; Score 3060.8; DB 10; Length 3143;
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Db 134 CTGAGCCCTCTGGCCCTTTCTCTTCCAACTGCTTCAAGTGTGCTGCGACGAC 193
QY 293 CGCGGGGAGCGGGGAGGGGCCCATGCCAGAGGTGAGATATGTCAGGGGATGAACG 352
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QY 353 TAGGCACTTAGCTTTCCACCAAGAGGGGCTCCAGGATTTGACACTCTGCTCCTGAG 412
Db 254 TAGGCACTTAGCTTTCCACCAAGAGGGGCTCCAGGATTTGACACTCTGCTCCTGAG 313
QY 413 TGGTGATGGAATACTCTACGTGGGGCTCGAGAGCCATTTGCGCTTGGATATCCA 472
Db 314 TGGTGATGGAATACTCTACGTGGGGCTCGAGAGCCATTTGCGCTTGGATATCCA 373
QY 473 GGATCCAGGGTCCCGAGGCTAAAGAACATGATACCGTGGCCAGCCAGTGACAGAAAAA 532
Db 374 GGATCCAGGGTCCCGAGGCTAAAGAACATGATACCGTGGCCAGCCAGTGACAGAAAAA 433
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QY 2393 AAGCAGAGAGCMAACCTCTCAGTCTCCCAAGGAATGAGGACCTCTGCGAGTGTGGA 2452
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QY 2453 CGCTGACAAACAACTGCTAGGCACTGAGTAGCTTAAACTCTAGGCACAGCCGGGCTG 2512
Db 2354 CGCTGACAAACAACTGCTAGGCACTGAGTAGCTTAAACTCTAGGCACAGCCGGGCTG 2413
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Db 3134 CTTA 3137
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RESULT 3

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US-10-015-395A-276
; Sequence 276, Application US/10015395A
; Publication No. US20040073015A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Baton, Dan J.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
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; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas P.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P28301C57
; CURRENT APPLICATION NUMBER: US/10/015,395A
; CURRENT FILING DATE: 2001-12-12
; Prior application removed - See file Wrapper or Palm
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 276
; LENGTH: 3143
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-015-395A-276
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Best Local Similarity 99.9%; Pred. No. 0;
Matches 3062; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Db 134 CTGAGCCCTCTGGGCCCTTTTCCCTTCCAACTGCTTCACTGCTGCTGCTGCGGACGAC 193
QY 293 CGCGGGGGAGCGCGGAGCGGCGCCATGCGCCAGGGTCAGATACATGATGAGGGGATGAACG 352
Db 194 CGCGGGGGAGCGCGGAGCGGCGCCATGCGCCAGGGTCAGATACATGAGGGGATGAACG 253
QY 353 TAGGGCACTTAGCTTCTTCCACAGAGGGCTCCAGGATTTTGACACTGTGCTTCCTGAG 412
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QY 533 GAGTGAATGTGCCCTTAAAGAGAGAGCAATGAGACAGAGTGTTCAACTTCATCCGTGT 592
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Db 554 TTGTACCTTCAATGAACCTTCAAGTCTTACCTGTTGCCCATCTCGGAGGACAGGTCAT 613
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US-10-013-907A-276
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; Publication No. US20030064925A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan I.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman

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; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2830P1C34
; CURRENT APPLICATION NUMBER: US/10/013,907A
; PRIORITY FILING DATE: 2001-12-10
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 276
; LENGTH: 3143
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-013-907A-276

Query Match      87.3%; Score 3060.8; DB 13; Length 3143;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 3062; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 173 AGAGTCTCCCTGGTGACAGTCTGTGGCTGAGCATGGCCCTCCAGGCCCTGGGCCCTGGACCC 232
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 2093 CTTTTCATACCCCTGTGATCTCTACTGAGTGGAGACCCAGACAGACCCCTGGCCCTGGA 2152
 1994 CTTTTCATACCCCTGTGATCTCTACTGAGTGGAGACCCAGACAGACCCCTGGCCCTGGA 2053
 2153 TCCTGAATCTGGCAGGATCCCGGGAGCATGTGAAGGTCCCGTTGACAGAGGTCACTGG 2212
 2054 TCCTGAATCTGGCAGGATCCCGGGAGCATGTGAAGGTCCCGTTGACAGAGGTCACTGG 2113
 2213 TGGGCGCCCTGGCTGCGCAGCAGTCTACTGCGCCCACTTTCTCACTGCTCACTGTCCT 2272
 2114 TGGGCGCCCTGGCTGCGCAGCAGTCTACTGCGCCCACTTTCTCACTGCTCACTGTCCT 2173
 2273 CTTTGCCTTAGTCTTTTCCAGAGCCCTCATCATCTCTGCTGGCCCTCCCATTTGAGACACT 2332
 2174 CTTTGCCTTAGTCTTTTCCAGAGCCCTCATCATCTCTGCTGGCCCTCCCATTTGAGACACT 2233
 2333 CCGGCTCGGGGCAAGTTTCAAGGCTGTGACACCTTGGCCCTGGCCCTGGGAGAGGCCCGTT 2392
 2234 CCGGCTCGGGGCAAGTTTCAAGGCTGTGACACCTTGGCCCTGGCCCTGGGAGAGGCCCGTT 2293
 2393 AAGCAGAGACAACCTTCCAGTCTCCCAAGGAATGACAGACCTTGCAGTGTATGGA 2452
 2294 AAGCAGAGACAACCTTCCAGTCTCCCAAGGAATGACAGACCTTGCAGTGTATGGA 2353
 2453 CGCTGACAACTGCTTAGCAGTGTGAGAGCTTAACTCTAGGCAAGCCCGGGCTG 2512
 2354 CGCTGACAACTGCTTAGCAGTGTGAGAGCTTAACTCTAGGCAAGCCCGGGCTG 2413
 2513 CGGTGACGACCTTGGCCATCTGCTGGGGGCGCCCAAGCAGACCTTGCAGTGTATGGA 2572
 2414 CGGTGACGACCTTGGCCATCTGCTGGGGGCGCCCAAGCAGACCTTGCAGTGTATGGA 2473
 2573 AGCAGCACAAGACCTTCTTCCCTGAGAGAGTCTTGTACTCTGCACTCACTGA 2632
 2474 AGCAGCACAAGACCTTCTTCCCTGAGAGAGTCTTGTACTCTGCACTCACTGA 2533
 2633 TGACACTCAGCAGGCTGATGACAGCAGTCTGCTCCCTATGGACTTCCCTTCTACCAA 2692
 2534 TGACACTCAGCAGGCTGATGACAGCAGTCTGCTCCCTATGGACTTCCCTTCTACCAA 2593
 2693 GCACATGAGTCTCTAAGAGGTGGGGGCTACCCCGAGACCTGCTCTACACTGATATTG 2752
 2594 GCACATGAGTCTCTAAGAGGTGGGGGCTACCCCGAGACCTGCTCTACACTGATATTG 2653
 2753 AAGAACTTGAAGAGTCTCTAAGAGGTGGGGGCTACCCCGAGACCTGCTCTACACTGATATTG 2812
 2654 AAGAACTTGAAGAGTCTCTAAGAGGTGGGGGCTACCCCGAGACCTGCTCTACACTGATATTG 2713
 2813 TTTCAAGAGACCTTAAACCTTCTGCTGCTCCAGGACCTTATGTAATGAACCAACAA 2872
 2714 TTTCAAGAGACCTTAAACCTTCTGCTGCTCCAGGACCTTATGTAATGAACCAACAA 2773
 2873 TCTAAACATCATATGCTAATGCTAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2932
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 2834 GGACACCAACCTTCTCCAGGCTCATGAGGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2893
 2993 ACCAGTGTGACCGCTGCTCCAGGAGTCTTCCCTGAGTCTGCTGAGTCTGCTGCTGCTGCT 3052
 2894 ACCAGTGTGACCGCTGCTCCAGGAGTCTTCTGAGTCTGCTGAGTCTGCTGCTGCTGCT 2953
 3053 TGCTTCAAGTGGGACAGTCTGATCCCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3112

2954 TGCTTCAGTTGGGCGCAGACTCTGATCCCTTCTGCTCCCTGGCAGATGGCAGGCTAATCTG 3013
 3113 AGCTTCTTCTCACTCCCTTTACCTAGTGCACCTTCACTCTCCCTCCCTCCCTTCTTCTT 3172
 3014 AGCTTCTTCTCACTCCCTTTACCTAGTGCACCTTCACTCTCCCTCCCTCCCTTCTTCTT 3073
 3173 GTTTTGGGATTCAGAAAACCTGCTTGTGAGAGTCTTCTTATTTTATTTTATTTTATTTTAAAG 3232
 3074 GTTTTGGGATTCAGAAAACCTGCTTGTGAGAGTCTTCTTATTTTATTTTATTTTATTTTAAAG 3133
 3233 CTTA 3236
 3134 CTTA 3137

RESULT 6
 US-10-015-499A-276
 ; Sequence 276, Application US/10015499A
 ; Publication No. US20030065142A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Botstein, David
 ; APPLICANT: Deshoyers, Luc
 ; APPLICANT: Eaton, Dan I.
 ; APPLICANT: Ferrara, Napoleone
 ; APPLICANT: Fong, Sherman
 ; APPLICANT: Gao, Wei-Qiang
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Grimaldi, Christopher J.
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Hillan, Kenneth J.
 ; APPLICANT: Pan, James
 ; APPLICANT: Paoni, Nicholas F.
 ; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 ; FILE OF INVENTION: Acids Encoding the Same
 ; FILE REFERENCE: P2830PIC42
 ; CURRENT APPLICATION NUMBER: US/10/015,499A
 ; Prior Filing DATE: 2001-12-11
 ; Prior Application removed - See File Wrapper or Palm
 ; NUMBER OF SEQ ID NOS: 477
 ; SEQ ID NO 276
 ; LENGTH: 3143
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; US-10-015-499A-276

Query Match 87.3%; Score 3060.8; DB 13; Length 3143;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 3062; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 173 AGAGTCCCTGGTGCAGTCTGTGGCTGAGCATGGCCCTCCAGCCCTGGGCCCTGGACCC 232
 DB 74 AGAGTCCCTGGTGCAGTCTGTGGCTGAGCATGGCCCTCCAGCCCTGGGCCCTGGACCC 133
 QY 233 CTGAGACCTCTGGGCCCTTTTCTTCTTCCAACTCTTCCAGTCTGCTGCTGCTGCTGCTGCTGCT 292
 DB 134 CTGAGACCTCTGGGCCCTTTTCTTCTTCCAACTCTTCCAGTCTGCTGCTGCTGCTGCTGCTGCT 193
 QY 293 CGCGGGGGAGCGCGGGGCGAGGGGCCCATGCCCCAGGGTCACTATGATGAGGGGATGAACG 352
 DB 194 CGCGGGGGAGCGCGGGGCGAGGGGCCCATGCCCCAGGGTCACTATGATGAGGGGATGAACG 253
 QY 353 TAGGGCACTTACCTTCTTCCACAGAGGGCCCTCCAGGATTTTGAACCTGCTGCTGCTGCTGCTGCTGCT 412
 DB 254 TAGGGCACTTACCTTCTTCCACAGAGGGCCCTCCAGGATTTTGAACCTGCTGCTGCTGCTGCTGCTGCT 313
 QY 413 TGGTATGGAATACTCTTCTACGTGGGGGCTCGAGAGACCATTTCTGCTGCTGCTGCTGCTGCTGCTGCT 472
 DB 314 TGGTATGGAATACTCTTCTACGTGGGGGCTCGAGAGACCATTTCTGCTGCTGCTGCTGCTGCTGCTGCT 373
 QY 473 GGATCCAGGGGCTCCCGAGGCTTAAGATCATGATACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 532

Db 374 GGATCCAGGGGTCCCCAGGCTAAAGAACATGATACCGTGGCCAGCCAGTGCACAGAAAAA 433
Qy 533 GAGTGAATGTGCCCTTTAAGAGAGAGCAATGAGACACAGTGTTCACACTTCATCCGGTGT 592
Db 434 GAGTGAATGTGCCCTTTAAGAGAGAGCAATGAGACACAGTGTTCACACTTCATCCGGTGT 493
Qy 593 CTTGGTCTTTTACAAATGTACCCATCTCTACACCTGGGACACCTTGGCCCTTCAGCCCTGC 652
Db 494 CTTGGTCTTTTACAAATGTACCCATCTCTACACCTGGGACACCTTGGCCCTTCAGCCCTGC 553
Qy 653 TTGTACCTTTCATTCGAACTTCAAGATTCTACTCTTGGCCATCTCGGAGACAAAGTTCAT 712
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Qy 713 GGAGGGAAGGCGCAAGCCCTTGGACCCCGCTCAACAGCATAGGCTGTCTTGTGGGA 772
Db 614 GGAGGGAAGGCGCAAGCCCTTGGACCCCGCTCAACAGCATAGGCTGTCTTGTGGGA 673
Qy 773 TGGGATGCTCTATTCTGTGTACTATGAACAACTTCTGGGAGTGGGCCCATCTGTATGCG 832
Db 674 TGGGATGCTCTATTCTGTGTACTATGAACAACTTCTGGGAGTGGGCCCATCTGTATGCG 733
Qy 833 CACACTGGGATCCAGGCTGTCTCAAGACGCAAACTTCTCGGCTGGCTGCATCATGA 892
Db 734 CACACTGGGATCCAGGCTGTCTCAAGACGCAAACTTCTCGGCTGGCTGCATCATGA 793
Qy 893 CGCCTCTTTTGTGGCAGCATCCCTTCGACCCAGTGTCTACTTCTTTCGAGGAGAC 952
Db 794 CGCCTCTTTTGTGGCAGCATCCCTTCGACCCAGTGTCTACTTCTTTCGAGGAGAC 853
Qy 953 AGCCAGCGAGTTTGAATCTTTGAGAGGCTCCACATTCGGGGTGGCTAGAGTCTGCAA 1012
Db 854 AGCCAGCGAGTTTGAATCTTTGAGAGGCTCCACATTCGGGGTGGCTAGAGTCTGCAA 913
Qy 1013 GAATGACGTGGCGCGGAAGAGTGTGCAAGAGTGGACCACTTCTTGAAGGCCCA 1072
Db 914 GAATGACGTGGCGCGGAAGAGTGTGCAAGAGTGGACCACTTCTTGAAGGCCCA 973
Qy 1073 GCTGCTCTGCCACCCAGCGGGGAGCTGCCCTTCAACGTCTATCCGCCACGCGTCTGCT 1132
Db 974 GCTGCTCTGCCACCCAGCGGGGAGCTGCCCTTCAACGTCTATCCGCCACGCGTCTGCT 1033
Qy 1133 CCGCGCGATCTTCCACAGCTCCCCACATCTAGCGAGTCTTACCTCCAGTGGCAGGT 1192
Db 1034 CCGCGCGATCTTCCACAGCTCCCCACATCTAGCGAGTCTTACCTCCAGTGGCAGGT 1093
Qy 1193 TGGCGGACACGAGGAGCTCTGGGTTTGTGCTTCTCTCTTGGACATTTGAACGTGTCTT 1252
Db 1094 TGGCGGACACGAGGAGCTCTGGGTTTGTGCTTCTCTCTTGGACATTTGAACGTGTCTT 1153
Qy 1253 TAAGGGGAATACAAAGAGTTGAACAAAGAACTTTCAGCTTGTGACTTATAGGGGCC 1312
Db 1154 TAAGGGGAATACAAAGAGTTGAACAAAGAACTTTCAGCTTGTGACTTATAGGGGCC 1213
Qy 1313 TGAGACCAACCCCGGCGAGGAGTGTCTAGTGGGCGCCCTCTCATAGGCGCCCTGAC 1372
Db 1214 TGAGACCAACCCCGGCGAGGAGTGTCTAGTGGGCGCCCTCTCATAGGCGCCCTGAC 1273
Qy 1373 CTTATGAAGGACCAATTTCTGTATGATGAGCAAGTGGTGGGAGCGCCCTCTGTGTGTGA 1432
Db 1274 CTTATGAAGGACCAATTTCTGTATGATGAGCAAGTGGTGGGAGCGCCCTCTGTGTGTGA 1333
Qy 1433 ATCTGGCTTGGAGTATACACGGCTTGCAGTGGAGACAGCCAGGCGCTTGTATGGGACAG 1492
Db 1334 ATCTGGCTTGGAGTATACACGGCTTGCAGTGGAGACAGCCAGGCGCTTGTATGGGACAG 1393
Qy 1493 CCATCTTGTATGTACTCTGGGAAACCAACAGGCTGTCTCCACAGGCTGTGTGTGTGA 1552
Db 1394 CCATCTTGTATGTACTCTGGGAAACCAACAGGCTGTCTCCACAGGCTGTGTGTGTGA 1453
Qy 1553 GGACAGCAGTGTCTCTGTGGAGAGATTCAGTGTCTTCCCTGACCTGACCTGTTTCG 1612
Db 1554 GGACAGCAGTGTCTCTGTGGAGAGATTCAGTGTCTTCCCTGACCTGACCTGTTTCG 1513

Qy 1613 CAACCTGAGCTGGCCCCCAACCCAGGCTGAGTGTGTAGGCTTCTCAGAGGTTGTCTG 1672
Db 1514 CAACCTGAGCTGGCCCCCAACCCAGGCTGAGTGTGTAGGCTTCTCAGAGGTTGTCTG 1573
Qy 1673 GAGGTTGCCCGAGCAAACTGTAGTGTCTATGAGAGCTGTGTGAGCTGTGTCTTGCCTG 1732
Db 1574 GAGGTTGCCCGAGCAAACTGTAGTGTCTATGAGAGCTGTGTGAGCTGTGTCTTGCCTG 1633
Qy 1733 GGACCCCACTGTGTGCTGGGACCTTGAATCTCCGAACTTGTGTCTTGTCTTGTCTTGCCTG 1792
Db 1634 GGACCCCACTGTGTGCTGGGACCTTGAATCTCCGAACTTGTGTCTTGTCTTGTCTTGCCTG 1693
Qy 1793 CTTGAACCTCTTGGAGAGGACATGAGCGGGGAAACCCAGAGTGGGATGTGCGAGTGG 1852
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Qy 1853 CCCCATGAGCAGGAGCCTTGGGCTTCAGAGCGCGCCGCAAACTCATTAAGAGTCTCTGCG 1912
Db 1754 CCCCATGAGCAGGAGCCTTGGGCTTCAGAGCGCGCCGCAAACTCATTAAGAGTCTCTGCG 1813
Qy 1913 TGTCCCTAACTCAATCTGGAGTCTCCCTGCCCCACCTGTGAGCTTGGGCTCTTATTA 1972
Db 1814 TGTCCCTAACTCAATCTGGAGTCTCCCTGCCCCACCTGTGAGCTTGGGCTCTTATTA 1873
Qy 1973 TTGGAGTCAATGCCCAGCAGCAGTCCCAAGAGCCTTCTTCACTGTCTCAATGGTCTCCT 2032
Db 1874 TTGGAGTCAATGCCCAGCAGCAGTCCCAAGAGCCTTCTTCACTGTCTCAATGGTCTCCT 1933
Qy 2033 CTTGCTGATGAGCAGGATGGAGTTGGGGTCTTACAGTGTCTGCGGCAACTGAGAAATGG 2092
Db 1934 CTTGCTGATGAGCAGGATGGAGTTGGGGTCTTACAGTGTCTGCGGCAACTGAGAAATGG 1993
Qy 2093 CTTTTTCATACCTGTGATCTCTACTGGGTGAGACAGCAGCAGCAGCAGCAGCAGCAG 2152
Db 1994 CTTTTTCATACCTGTGATCTCTACTGGGTGAGACAGCAGCAGCAGCAGCAGCAGCAG 2053
Qy 2153 TCTGAACTGGGAGCAGTCCCCCGGAGCATGTGAGGTCCCGTTGACAGGAGTCAAGTGG 2212
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Qy 2213 TGGGGCGGCTGGGTGCGCCAGCAGTCTTACTTGGGCCCACTTTGTCACTGTCACTGTCT 2272
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Qy 2333 CCGGGCTGGGGCAAGTTTCAGGCTGTGAGACCTTGGGCCCTGGGGAGAGGCCCCGTT 2392
Db 2234 CCGGGCTGGGGCAAGTTTCAGGCTGTGAGACCTTGGGCCCTGGGGAGAGGCCCCGTT 2293
Qy 2393 AAGCAGAGAGCAACCTCCAGTCTCCCAAGGAAATGCGAGGACCTCTGCGAGTGTGTGA 2452
Db 2294 AAGCAGAGAGCAACCTCCAGTCTCCCAAGGAAATGCGAGGACCTCTGCGAGTGTGTGA 2353
Qy 2453 CGCTGACAACTCTAGGCACTAGGTAGCTTAACTCTAGGCAAGGCGCGGGCTG 2512
Db 2354 CGCTGACAACTCTAGGCACTAGGTAGCTTAACTCTAGGCAAGGCGCGGGCTG 2413
Qy 2513 CGGTGAGGACCTTGGCCATGTGGTGGCGCGGCCAAGCAAGCAGCCTGACTAGGATGAC 2572
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Qy 2573 AGCAGCAGAAAGACCACTTCTCCCTGAGAGAGCTTCTGCTACTCTGATCACTGA 2632
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Qy 2633 TGAACCTCAGCAGGAGTGCACAGCAGTCTGCCCTCCCCCTATGGGACTCCCTTCTACCAA 2692
Db 2534 TGAACCTCAGCAGGAGTGCACAGCAGTCTGCCCTCCCCCTATGGGACTCCCTTCTACCAA 2593


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QY 2693 GCACATGAGCTCTTAACAGAGGTGGGGCTACCCCGAGACCTGCTCTACACTGATATTG 2752
Db 2594 GCACATGAGCTCTTAACAGAGGTGGGGCTACCCCGAGACCTGCTCTACACTGATATTG 2653
QY 2753 AAGAACCTGGAGAGGATCTTTCAGTTCCTGGSCATTCAGGAGACCTCCAGAAAACACAGTG 2812
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QY 2813 TTTCAAGAGACCTTAACAAACCTGCTGCTCCAGGACCTTATGGTAATGAACACCAACA 2872
Db 2714 TTTCAAGAGACCTTAACAAACCTGCTGCTCCAGGACCTTATGGTAATGAACACCAACA 2773
QY 2873 TCTAAACAATCATATGCTAAACATGCCACTCTGCGAAACTCCACTCTGAAGCTGCCGCTTT 2932
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QY 3113 AGCTTCTTCACTCTTACCTTACCTAGCTGACCCCTTCACTCTCCCTCTCCCTTTCT 3172
Db 3014 AGCTTCTTCACTCTTACCTTACCTAGCTGACCCCTTCACTCTCCCTCTCCCTTTCT 3073
QY 3173 GTTTTGGGATTCAGAAACTGCTTGTGACAGACTGTTTATTTTATTTAAATAAAG 3232
Db 3074 GTTTTGGGATTCAGAAACTGCTTGTGACAGACTGTTTATTTTATTTAAATAAAG 3133
QY 3233 CTTA 3236
Db 3134 CTTA 3137
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RESULT 7

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US-10-226-254A-276
; Sequence 276, Application US/10226254A
; Publication No. US20030224478A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan I.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2830F1C68
; CURRENT APPLICATION NUMBER: US/10/226,254A
; PRIOR FILING DATE: 2002-08-21
; PRIOR APPLICATION NUMBER: 60/098716
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098723
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098749
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098750
; PRIOR FILING DATE: 1998-09-01
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; PRIOR APPLICATION NUMBER: 60/098803
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/098821
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/098843
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/099536
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099596
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099598
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 276
; LENGTH: 3143
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-226-254A-276

Query Match      87.3%; Score 3060.8; DB 13; Length 3143;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 3062; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 173 AGAGTCCTCCTGGTGACAGTCTGTGGCTGAGCATGGCCCTCCAGCCCTGGGCCCTGGACCC 232
Db 74 AGAGTCCTCCTGGTGACAGTCTGTGGCTGAGCATGGCCCTCCAGCCCTGGGCCCTGGACCC 133
QY 233 CTGAGAGCTCTCGGGCCCTTTTCCCTTCCACTGCTTTCAGCTGCTGCTGCGGACGAC 292
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QY 293 CGCGGGGGAGCGCGGCGAGGGGCCCATGCCCAGGGTTCAGATATCTATGACGGGGATGAACG 352
Db 194 CGCGGGGGAGCGCGGCGAGGGGCCCATGCCCAGGGTTCAGATATCTATGACGGGGATGAACG 253
QY 353 TAGGGCACTTAGCTTCTTCCACAGAGAGGGCCCTCCAGGATTTTGACACTCTGCTCCTGAG 412
Db 254 TAGGGCACTTAGCTTCTTCCACAGAGAGGGCCCTCCAGGATTTTGACACTCTGCTCCTGAG 313
QY 413 TGGTGATGGAATAACTCTCTACGTGGGGGCTCGAGAAAGCCATTCTGGCCCTTGATATCCA 472
Db 314 TGGTGATGGAATAACTCTCTACGTGGGGGCTCGAGAAAGCCATTCTGGCCCTTGATATCCA 373
QY 473 GGATCCAGGGTCCCGAGGCTTAAGAAACATGATACCTGGCCAGCCAGTGACAGAAAAA 532
Db 374 GGATCCAGGGTCCCGAGGCTTAAGAAACATGATACCTGGCCAGCCAGTGACAGAAAAA 433
QY 533 CAGTGAATGTGCTTTTAAAGAAAGAGCAATGAGACACAGTGTTCAACTTCATCCCTGT 592
Db 434 CAGTGAATGTGCTTTTAAAGAAAGAGCAATGAGACACAGTGTTCAACTTCATCCCTGT 493
QY 593 CTTGGTTTCTTAATGTCAACCTCCATCTACCTCGGGACCTTCGCCCTTCAGCCCTGC 652
Db 494 CTTGGTTTCTTAATGTCAACCTCCATCTACCTCGGGACCTTCGCCCTTCAGCCCTGC 553
QY 653 TTGTACCTTCAATGAATCTCAAGATTCCTACCTGTTCCCATCTCGGAGACAGAGTCA 712
Db 554 TTGTACCTTCAATGAATCTCAAGATTCCTACCTGTTCCCATCTCGGAGACAGAGTCA 613
QY 713 GGAGGAAAAAGGCCAAAGCCCTTTGACCCCGCTCAAGCATACGCTGTCTTGTGTGA 772
Db 614 GGAGGAAAAAGGCCAAAGCCCTTTGACCCCGCTCAAGCATACGCTGTCTTGTGTGA 673
QY 773 TGGGATGCTCTATTCTGTATGAACCTTCCCTGGCAGTGAGCCCATCTGATGCG 832
Db 674 TGGGATGCTCTATTCTGTATGAACCTTCCCTGGCAGTGAGCCCATCTGATGCG 733
QY 833 CACACTGGATCCAGCTGTCTCAAGACGCAACTTCTCCGCTGGTGTGATCATGA 892
Db 734 CACACTGGATCCAGCTGTCTCAAGACGCAACTTCTCCGCTGGTGTGATCATGA 793
QY 893 CGCCTCCTTTGTGCGACCCATCCCTTCGACCCAGGTGCTCTACTTCTTCTCGGAGAC 952
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Db 794 |||||CGCTCTTTTGTGGCAGCATTCCCTTCGACCCAGGTGGTCTACTTCTTCGAGGAGAC 853
Qy 953 AGCCAGCAGATTGACTTCTTTGAGAGCTCCACACATCGCGGTGGCTAGTCTGCAG 1012
Db 854 AGCCAGCAGATTGACTTCTTTGAGAGCTCCACACATCGCGGTGGCTAGTCTGCAG 913
Qy 1013 GAAATGAGCTGGCGCGGAGAAAGCTGTCTGCAAGAGTGGACACCTTCTCTGAAGGCCCA 1072
Db 914 GAAATGAGCTGGCGCGGAGAAAGCTGTCTGCAAGAGTGGACACCTTCTCTGAAGGCCCA 973
Qy 1073 GCTGCTGTGACCCAGCAGCGCGGAGCTGCCCTTCAACGTCATCGCCACGCGTCTGTCT 1132
Db 974 GCTGCTGTGACCCAGCAGCGCGGAGCTGCCCTTCAACGTCATCGCCACGCGTCTGTCT 1033
Qy 1133 CCGCGCGATTCTCCACAGCTCCCAATCTGACAGTCTTACGCTGGACTTACTTATAGGGCCC 1192
Db 1034 CCGCGCGATTCTCCACAGCTCCCAATCTGACAGTCTTACGCTGGACTTACTTATAGGGCCC 1093
Qy 1193 TGGCGGACACGAGAGCTCTGCGGTTTGTGCTTCTCTCTTGGACATTAAGAGTGTCTT 1252
Db 1094 TGGCGGACACGAGAGCTCTGCGGTTTGTGCTTCTCTCTTGGACATTAAGAGTGTCTT 1153
Qy 1253 TAAGGGGAATACAAAGATTGAACAAAGAACTTACGCTGGACTTACTTATAGGGCCC 1312
Db 1154 TAAGGGGAATACAAAGATTGAACAAAGAACTTACGCTGGACTTACTTATAGGGCCC 1213
Qy 1313 TGAGACCAACCCCGGCCAGCAGTTGCTCAGTGGGCCCCCTCTCTGATAGGCCCCTGAC 1372
Db 1214 TGAGACCAACCCCGGCCAGCAGTTGCTCAGTGGGCCCCCTCTCTGATAGGCCCCTGAC 1273
Qy 1373 CTTGATGAAGACCAATTTCTGATGGATGACAAAGTGGTGGGAGCGCCCTCTGTGTGAA 1432
Db 1274 CTTGATGAAGACCAATTTCTGATGGATGACAAAGTGGTGGGAGCGCCCTCTGTGTGAA 1333
Qy 1433 ATCTGGCGTGGAGTATACACGGCTTGCAATGGAGACAGCCAGGCGCTTGTATGGGCACAG 1492
Db 1334 ATCTGGCGTGGAGTATACACGGCTTGCAATGGAGACAGCCAGGCGCTTGTATGGGCACAG 1393
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Qy 1613 CAACCTGAGCTGGCCCCCAGGCTGAGTGTGTTAGGCTTCTCAGAGGTGTCTG 1672
Db 1514 CAACCTGAGCTGGCCCCCAGGCTGAGTGTGTTAGGCTTCTCAGAGGTGTCTG 1573
Qy 1673 GAGGCTGCCGAGCCAACTGTAGTGTCTATGAGAGCTGTGTGACTGTCTCTTGGCCG 1732
Db 1574 GAGGCTGCCGAGCCAACTGTAGTGTCTATGAGAGCTGTGTGACTGTGTCTTGGCCG 1633
Qy 1733 GGACCCCACTGTGCTGGGACCTTGAAGTCCGAACTGTTGCCCTCTCTGTCTGCCCCCAA 1792
Db 1634 GGACCCCACTGTGCTGGGACCTTGAAGTCCGAACTGTTGCCCTCTCTGTCTGCCCCCAA 1693
Qy 1793 CCTGAATCTCTGGAAGCAGGACATGGAGCGGGGAAACCCAGAGTGGGACATGTGCCAGTGG 1852
Db 1694 CCTGAATCTCTGGAAGCAGGACATGGAGCGGGGAAACCCAGAGTGGGACATGTGCCAGTGG 1753
Qy 1853 CCCATGAGCAGGAGCTTCCGCTCAGAGCGCGCCGAAATCAATTAAGAGTCTCTGGC 1912
Db 1754 CCCATGAGCAGGAGCTTCCGCTCAGAGCGCGCCGAAATCAATTAAGAGTCTCTGGC 1813
Qy 1913 TGTCCCTAACTCTGAGTCTCCCTTGGCCCACTGTGAGCTTGGCTTATTA 1972
Db 1814 TGTCCCACTCTCTGAGTCTCCCTTGGCCCACTGTGAGCTTGGCTTATTA 1873
Qy 1973 TTGAGTCTATGSCCCAGCAGAGTCCCAAGAGCTCTTCCACTGTCTACATAGTCTCCCT 2032

Db 1874 TTGGAGTCATGSCCCAGCAGCAGTCCCAGAGAGCTCTTCCACTGTCTACATGGCTCCCT 1933
Qy 2033 CTTGCTGATAGTGCAGGATGGAGTTGGGGTCTCTACCAAGTCTGGGCAACTGAGAAATGG 2092
Db 1934 CTTGCTGATAGTGCAGGATGGAGTTGGGGTCTCTACCAAGTCTGGGCAACTGAGAAATGG 1993
Qy 2093 CTTTTCATACCTGTGATCTCTCTACTGAGTGGACAGCAGGACCAAGACCTTGGCCCTTGA 2152
Db 1994 CTTTTCATACCTGTGATCTCTCTACTGAGTGGACAGCAGGACCAAGACCTTGGCCCTTGA 2053
Qy 2153 TCTGAACTGGCAGGATCTCCCGGAGCATGTGAAGTCCGTTTGAACAGGTCAGTGG 2212
Db 2054 TCTGAACTGGCAGGATCTCCCGGAGCATGTGAAGTCCGTTTGAACAGGTCAGTGG 2113
Qy 2213 TGGGGCCGCTGGCTGGCCAGCAGTCTCTACTGGGCCCACTTTGTCACTGTCTGTCT 2272
Db 2114 TGGGGCCGCTGGCTGGCCAGCAGTCTCTACTGGGCCCACTTTGTCACTGTCTGTCT 2173
Qy 2273 CTTTGGCTTGTGCTTTCAGGAGCCTCATCATCTCTGTGGCTCCCAATTGAGAGCACT 2332
Db 2174 CTTTGGCTTGTGCTTTCAGGAGCCTCATCATCTCTGTGGCTCCCAATTGAGAGCACT 2233
Qy 2333 CCGGGCTCGGGCAAGGTTTTCAGGCTGTGAGACCTCGCCCTGGGAGAGGCCCCGTT 2392
Db 2234 CCGGGCTCGGGCAAGGTTTTCAGGCTGTGAGACCTCGCCCTGGGAGAGGCCCCGTT 2293
Qy 2393 AAGCAGAGAGCAACCTCCTCAGTCTCCAGGAATGAGGACCTCTGCGAGTGTGGA 2452
Db 2294 AAGCAGAGAGCAACCTCCTCAGTCTCCAGGAATGAGGACCTCTGCGAGTGTGGA 2353
Qy 2453 CGCTGACAACTGCTAGGCACTGAGTGTAACTTCTAGGACAGGCGGGGCTG 2512
Db 2354 CGCTGACAACTGCTAGGCACTGAGTGTAACTTCTAGGACAGGCGGGGCTG 2413
Qy 2513 CGGTGAGGACACTGTGGCTGTGGCGGCCCAAGCAGACAGCCCTGACTAGGATGAC 2572
Db 2414 CGGTGAGGACACTGTGGCTGTGGCGGCCCAAGCAGACAGCCCTGACTAGGATGAC 2473
Qy 2573 AGCAGCAAAAGACCACTTCTCCCTGAGAGAGCTTCTGCTACTCTGATCAGTGA 2632
Db 2474 AGCAGCAAAAGACCACTTCTCCCTGAGAGAGCTTCTGCTACTCTGATCAGTGA 2533
Qy 2633 TGACACTCAGCAGGCTGATGACAGCAGTCTCCCTCCCTATGGGACTCCCTTCTACCAA 2692
Db 2534 TGACACTCAGCAGGCTGATGACAGCAGTCTCCCTCCCTATGGGACTCCCTTCTACCAA 2593
Qy 2693 GCACATGAGCTCTTAAACAGGCTGGGGCTACCCCGAGCCTGCTCCTACACTGATATG 2752
Db 2594 GCACATGAGCTCTTAAACAGGCTGGGGCTACCCCGAGCCTGCTCCTACACTGATATG 2653
Qy 2753 AAGAACCTGGAGAGGATCCTTCAGTCTGGCCCATTCAGGGGACCTCCAGAAACACAGTG 2812
Db 2654 AAGAACCTGGAGAGGATCCTTCAGTCTGGCCCATTCAGGGGACCTCCAGAAACACAGTG 2713
Qy 2813 TTTCAAGAGACCTTAAAAACCTGCTGTCAGGACCTATGGTAATGAAACCAAAACA 2872
Db 2714 TTTCAAGAGACCTTAAAAACCTGCTGTCAGGACCTATGGTAATGAAACCAAAACA 2773
Qy 2873 TCTTAAACATCATATGCTAACTGACCTCTGGAACCTCCACTCTGAGCTGCGCTTT 2932
Db 2774 TCTTAAACATCATATGCTAACTGACCTCTGGAACCTCCACTCTGAGCTGCGCTTT 2833
Qy 2933 GGAACCAACACTCCCTTCTCCAGGCTCATGAGGATCTGCTCCCTCTCTTCCCTT 2992
Db 2834 GGAACCAACACTCCCTTCTCCAGGCTCATGAGGATCTGCTCCCTCTCTTCCCTT 2893
Qy 2993 ACCAGTGTGCAACCTGACTCCAGGAGTCTTCCCTGAACTCTGACACCTTCTTCT 3052
Db 2894 ACCAGTGTGCAACCTGACTCCAGGAGTCTTCCCTGAACTCTGACACCTTCTTCT 2953
Qy 3053 TGCTTCAGTTGGGCGAGACTCTGATCCCTTCTGCCCCGAGAAATGGCAGGGTATCTG 3112
Db 2954 TGCTTCAGTTGGGCGAGACTCTGATCCCTTCTGCCCCGAGAAATGGCAGGGTATCTG 3013

Best Local Similarity 99.98; Pred. No. 0; Matches 3062; Conservative				Mismatches 2; Indels 0; Gaps 0;			
QY	173	AGAGTCCCTGGTGACAGTCTGTGGCTGACATGGCCCTCCAGCCCTCGGCTCGAACCC	232	QY	1253	TAAGGGAAATACAAAGAGTTGAACAAAGAAACTTACGCTGGACTACTTATAGGGCCCC	1312
DB	74	AGAGTCCCTGGTGACAGTCTGTGGCTGACATGGCCCTCCAGCCCTCGGCTCGAACCC	133	DB	1154	TAAGGGAAATACAAAGAGTTGAACAAAGAAACTTACGCTGGACTACTTATAGGGCCCC	1213
QY	233	CTGAGCTCCTGGGCTTTTCTCTTCCAACTGCTTCAAGTCTGCTGCTGCCAGCAGAC	292	QY	1313	TGAGACAAACCCCGCCAGGAGTTGCTCAGTGGGCCCCCTCTCTGATTAAGGCCCTGAC	1372
DB	134	CTGAGCTCCTGGGCTTTTCTCTTCCAACTGCTTCAAGTCTGCTGCTGCCAGCAGAC	193	DB	1214	TGAGACAAACCCCGCCAGGAGTTGCTCAGTGGGCCCCCTCTCTGATTAAGGCCCTGAC	1273
QY	293	CGCGGGGGAGGGGGCAGGGGCCATGCCAGGGTCAGATATAGCAGGGGATGAAGC	352	QY	1373	CTTCATGAAGAACCAATTTCTCTGATGAGCAAGTGGTGGGACGCCCTCTGTGTGAA	1432
DB	194	CGCGGGGGAGGGGGCAGGGGCCATGCCAGGGTCAGATATAGCAGGGGATGAAGC	253	DB	1274	CTTCATGAAGAACCAATTTCTCTGATGAGCAAGTGGTGGGACGCCCTCTGTGTGAA	1333
QY	353	TAGGGCACTTAGCTTCTTCCACAGAGAGGCCCTCCAGGATTTTGACACTCTGCTCTGAG	412	QY	1433	ATCTGGCGTGGAGTATACAGCGCTTGAGTGGAGACAGCCAGGGCTTGTATGGGACAG	1492
DB	254	TAGGGCACTTAGCTTCTTCCACAGAGAGGCCCTCCAGGATTTTGACACTCTGCTCTGAG	313	DB	1334	ATCTGGCGTGGAGTATACAGCGCTTGAGTGGAGACAGCCAGGGCTTGTATGGGACAG	1393
QY	413	TGGTATGGAAATACTCTCTACGTGGGGCTCGAGAGCAATTTCTGGCTTGGATATCA	472	QY	1493	CAATCTGTCTATGTACCTGGGAAACACACAGAGGTCTCTCCACAAGGCTGTGGTAAGTGG	1552
DB	314	TGGTATGGAAATACTCTCTACGTGGGGCTCGAGAGCAATTTCTGGCTTGGATATCA	373	DB	1394	CAATCTGTCTATGTACCTGGGAAACACACAGAGGTCTCTCCACAAGGCTGTGGTAAGTGG	1453
QY	473	GGATCCAGGGGTCCCCAGGCTAAAGAACATGATACCGTGGCCAGCCAGTGACAGAAAAA	532	QY	1553	GGACAGAGTGTCTCATCTGGTGGAGAGATTACGCTGTTCCCTGACCCCTGAACTGTTCG	1612
DB	374	GGATCCAGGGGTCCCCAGGCTAAAGAACATGATACCGTGGCCAGCCAGTGACAGAAAAA	433	DB	1454	GGACAGAGTGTCTCATCTGGTGGAGAGATTACGCTGTTCCCTGACCCCTGAACTGTTCG	1513
QY	533	GAGTGAATGTCCTTTAAGAGAGAGCAATGAGACACAGTGTTCAACTTCACTCCGTGT	592	QY	1613	CAACTGCAGCTGGCCCCCACCAGGGTGCAGTGTGTTGTAGGCTTCTCAGAGGTGTCTG	1672
DB	434	GAGTGAATGTCCTTTAAGAGAGAGCAATGAGACACAGTGTTCAACTTCACTCCGTGT	493	DB	1514	CAACTGCAGCTGGCCCCCACCAGGGTGCAGTGTGTTGTAGGCTTCTCAGAGGTGTCTG	1573
QY	593	CCTGGTTCCTTACAATGTCAACCCATCTCTACACTGCGGACCTTCGCTTCAGCCCTGC	652	QY	1673	GAGGTGCCCCAGCCAACTGTAGTGTCTATGAGAGTGTGTGCACTGTGTCTTGCCTG	1732
DB	494	CCTGGTTCCTTACAATGTCAACCCATCTCTACACTGCGGACCTTCGCTTCAGCCCTGC	553	DB	1574	GAGGTGCCCCAGCCAACTGTAGTGTCTATGAGAGTGTGTGCACTGTGTCTTGCCTG	1633
QY	653	TTGTACCTTCATTGAACCTCAAGATTCCTACCTGTTGCCATCTCGAGAGCAAGTCAAT	712	QY	1733	GGACCCCACTGTGCTGGGACCTGAGTCCCGAACCTGTGCTCTCTGCTGCCCCCAA	1792
DB	554	TTGTACCTTCATTGAACCTCAAGATTCCTACCTGTTGCCATCTCGAGAGCAAGTCAAT	613	DB	1634	GGACCCCACTGTGCTGGGACCTGAGTCCCGAACCTGTGCTCTCTGCTGCCCCCAA	1693
QY	713	GGAGGAAAGGGCCAAAGCCCCCTTTGACCCCGCTCAAGCATACCGGCTGTCTGTGTGA	772	QY	1793	CCTGAACTCTCTGGAAGCAGGACATGAGAGCGGGGAAACCCAGAGTGGGCATGTGCCAGTGG	1852
DB	614	GGAGGAAAGGGCCAAAGCCCCCTTTGACCCCGCTCAAGCATACCGGCTGTCTGTGTGA	673	DB	1694	CCTGAACTCTCTGGAAGCAGGACATGAGAGCGGGGAAACCCAGAGTGGGCATGTGCCAGTGG	1753
QY	773	TGGATGCTCTATTCTGGTACTATGAACAACTTCTCGGGAGTGGGCCATCTCTGATGCG	832	QY	1853	CCCATGAGCAGAGAGCTTGGCCCTCAGAGCGCCCGCCCAATCATTAAGAAGTCTCTGGC	1912
DB	674	TGGATGCTCTATTCTGGTACTATGAACAACTTCTCGGGAGTGGGCCATCTCTGATGCG	733	DB	1754	CCCATGAGCAGAGAGCTTGGCCCTCAGAGCGCCCGCCCAATCATTAAGAAGTCTCTGGC	1813
QY	833	CACACTGGGATCCAGGCTGTCTCAAGACCGACAACTTCTCCGCTGGTGTGATCATGA	892	QY	1913	TGTCCCTAACTCCATCTCTGGAGTCCCTGCCCCCACTGTGACGCTTGGCCTCTTATTA	1972
DB	734	CACACTGGGATCCAGGCTGTCTCAAGACCGACAACTTCTCCGCTGGTGTGATCATGA	793	DB	1814	TGTCCCAACTCCATCTCTGGAGTCCCTGCCCCCACTGTGACGCTTGGCCTCTTATTA	1873
QY	893	CGCCTCTTTGTGSCAGCCATCCCTTCGACCCAGGTGCTCTACTTCTTCTCGAGGAGAC	952	QY	1973	TTGAGTCTATGCCCCAGCAGCAGTCCAGAGGCTCTTCCACTGTCTACATGGCTCCCT	2032
DB	794	CGCCTCTTTGTGSCAGCCATCCCTTCGACCCAGGTGCTCTACTTCTTCTCGAGGAGAC	853	DB	1874	TTGAGTCTATGCCCCAGCAGCAGTCCAGAGGCTCTTCCACTGTCTACATGGCTCCCT	1933
QY	953	AGCCAGAGGTTGACCTTTTGAGAGGCTCCACATCCGGGTGGCTAGAGTCTGCAA	1012	QY	2033	CTTGTCTATGATGAGGATGGAGTTGGGGTCTCTACAGTGTCTGGGCAACTGAGAAATGG	2092
DB	854	AGCCAGAGGTTGACCTTTTGAGAGGCTCCACATCCGGGTGGCTAGAGTCTGCAA	913	DB	1934	CTTGTCTATGATGAGGATGGAGTTGGGGTCTCTACAGTGTCTGGGCAACTGAGAAATGG	1993
QY	1013	GAATGACGTGGGCGGAAAGCTGTCTGAGAGAGAGTGGACCACTTCTGAAAGCCCA	1072	QY	2093	CTTTTCATACCTGTGATCTCTACTAGGTGGAGCAGCAGGACAGACCTTGGCCCTGGA	2152
DB	914	GAATGACGTGGGCGGAAAGCTGTCTGAGAGAGAGTGGACCACTTCTGAAAGCCCA	973	DB	1994	CTTTTCATACCTGTGATCTCTACTAGGTGGAGCAGCAGGACAGACCTTGGCCCTGGA	2053
QY	1073	GCTGCTCTGACCCAGCGGGGAGCTGCCCTTCAAGCTCATCCGCCAGCGGTCTGTCT	1132	QY	2153	TCCTGAACTGGCAGGCATCCCGCGGAGCATGTGAAGGTCCCGTTGACAGGGTCAGTGG	2212
DB	974	GCTGCTCTGACCCAGCGGGGAGCTGCCCTTCAAGCTCATCCGCCAGCGGTCTGTCT	1033	DB	2054	TCCTGAACTGGCAGGCATCCCGCGGAGCATGTGAAGGTCCCGTTGACAGGGTCAGTGG	2113
QY	1133	CCCCCGGATTTCTCCACAGCTCCCCACATCTAGCAGTCTTCACTTCCAGTGGCAGGT	1192	QY	2213	TGGGGCCGCTGGCTGCCAGAGTCTCTACTGGCCCCCACTTTGTCTACTGTCTCTCT	2272
DB	1034	CCCCCGGATTTCTCCACAGCTCCCCACATCTAGCAGTCTTCACTTCCAGTGGCAGGT	1093	DB	2114	TGGGGCCGCTGGCTGCCAGAGTCTCTACTGGCCCCCACTTTGTCTACTGTCTCTCT	2173
QY	1193	TGGGGGACAGAGCTCTGGGTTTGTGCTTCTCTCTTGGACATTTGAACGTGTCTT	1252	QY	2273	CTTTGGCTTTAGTGTCTTTCAGGAGCCCTCATCATCTCTGTGGCTTCCCCCATTTGAGAGCACT	2332
DB				DB	2174	CTTTGGCTTTAGTGTCTTTCAGGAGCCCTCATCATCTCTGTGGCTTCCCCCATTTGAGAGCACT	2293

QY 2333 CCGGCTCGGGCAAGGTTCAAGGGCTGTGAGACCTCTGGCCCTCGGGAGAAAGGCCCGTT 2392
DB 2234 CCGGCTCGGGCAAGGTTCAAGGGCTGTGAGACCTCTGGCCCTCGGGAGAAAGGCCCGTT 2293
QY 2393 AAGCAGAGAGCAACACCTCCAGTCTCCCAAGGAATGACAGACCTCTGCCAGTGATGTGA 2452
DB 2294 AAGCAGAGAGCAACACCTCCAGTCTCCCAAGGAATGACAGACCTCTGCCAGTGATGTGA 2353
QY 2453 CGCTGACAAACCTCGCTAGGCACTGAGGTAGCTTAAACTCTAGGCACAGGCCCGGGCTG 2512
DB 2354 CGCTGACAAACCTCGCTAGGCACTGAGGTAGCTTAAACTCTAGGCACAGGCCCGGGCTG 2413
QY 2513 CGGTGACGACCTCGCTGCTGCTGCGGGCCCAAGCAGACCTCTGCTAGCTAGCATGAC 2572
DB 2414 CGGTGACGACCTCGCTGCTGCTGCGGGCCCAAGCAGACCTCTGCTAGCTAGCATGAC 2473
QY 2573 AGCAGCAAAAGACCACTTCTCCCTGAGAGAGCTTCTGCTAGCTAGCATGAC 2632
DB 2474 AGCAGCAAAAGACCACTTCTCCCTGAGAGAGCTTCTGCTAGCTAGCATGAC 2533
QY 2633 TGACACTGACAGGCTGATGACAGCAGTCTGCTCCCTATGGGACTCCCTTACCAA 2692
DB 2534 TGACACTGACAGGCTGATGACAGCAGTCTGCTCCCTATGGGACTCCCTTACCAA 2593
QY 2693 GCACATGAGCTCTTAACAGGCTGGGGCTACCCCGACACCTGCTCTTACACTGATTTG 2752
DB 2594 GCACATGAGCTCTTAACAGGCTGGGGCTACCCCGACACCTGCTCTTACACTGATTTG 2653
QY 2753 AGRACCTGAGAGGATCTTTCAGTCTTGGCCATTCAGGAGCCCTCCAGAAACACACAGT 2812
DB 2654 AGRACCTGAGAGGATCTTTCAGTCTTGGCCATTCAGGAGCCCTCCAGAAACACACAGT 2713
QY 2813 TTTCAAGAGACCTTAAACAACTGCTGTCCAGGACCTTATGTAATGAACACCAACA 2872
DB 2714 TTTCAAGAGACCTTAAACAACTGCTGTCCAGGACCTTATGTAATGAACACCAACA 2773
QY 2873 TCTAAACATCATATGCTTAACATGACCTCTCTGGAACCTCACTCTGAAGCTGGGCTTT 2932
DB 2774 TCTAAACATCATATGCTTAACATGACCTCTCTGGAACCTCACTCTGAAGCTGGGCTTT 2833
QY 2933 GGACACCAACACTCCCTTCTCCAGGCTCATGACAGGATCTGCTCCCTCTGCTTCCCTT 2992
DB 2834 GGACACCAACACTCCCTTCTCCAGGCTCATGACAGGATCTGCTCCCTCTGCTTCCCTT 2893
QY 2993 ACCAGTCTGACCGCTGACCTCCAGGAGTCTTCCCTGAAGTCTGACCACTTCTTCT 3052
DB 2894 ACCAGTCTGACCGCTGACCTCCAGGAGTCTTCTTCTGAAGTCTGACCACTTCTTCT 2953
QY 3053 TGCTTCAGTTGGGGAGACTCTGATCCCTTCTGCTGCTGAGATGGGAGTAACTG 3112
DB 2954 TGCTTCAGTTGGGGAGACTCTGATCCCTTCTGCTGCTGAGATGGGAGTAACTG 3013
QY 3113 AGCCTTCTTCACTCCCTTACCTAGTACCTTCTGCTGCTGCTGCTGCTGCTGCTT 3172
DB 3014 AGCCTTCTTCACTCCCTTACCTAGTACCTTCTGCTGCTGCTGCTGCTGCTT 3073
QY 3173 GTTTTGGGATTCAGAAACCTGCTGTCAGAGACTGTTATTTTATTAATAAATATAGG 3232
DB 3074 GTTTTGGGATTCAGAAACCTGCTGTCAGAGACTGTTATTTTATTAATAAATATAGG 3133
QY 3233 CTTA 3236
DB 3134 CTTA 3137

RESULT 10

US-10-015-393A-276
; Sequence 276, Application US/10015393A
; Publication No. US2003069179A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David

APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2830P1C46
; CURRENT APPLICATION NUMBER: US/10/015,393A
; CURRENT FILING DATE: 2002-06-10
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 276
; LENGTH: 3143
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-015-393A-276

Query Match 87.3%; Score 3060.8; DB 15; Length 3143;

Best Local Similarity 99.9%; Pred. No. 0;

Matches 3062; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 173 AGAGCTCCCTGTGTGACAGTCTGTGGCTGAGCATGGCCCTCCAGCCCTGGGCTGACCC 232
DB 74 AGAGCTCCCTGTGTGACAGTCTGTGGCTGAGCATGGCCCTCCAGCCCTGGGCTGACCC 133
QY 233 CTGGAGCTCTCTGGGCTTTTCTCTTCCAACTGTCTCAGCTCTGCTCTCCGACGAC 292
DB 134 CTGGAGCTCTCTGGGCTTTTCTCTTCCAACTGTCTCAGCTCTGCTCTCCGACGAC 193
QY 293 CGGGGGGAGGGGGGAGGG 352
DB 194 CGGGGGGAGGGGGGAGGG 253
QY 353 TAGGGCACTTAGCTTCTTCCACAGAGGGGCTTCCAGGATTTTGACACTCTCTCTGAG 412
DB 254 TAGGGCACTTAGCTTCTTCCACAGAGGGGCTTCCAGGATTTTGACACTCTCTCTGAG 313
QY 413 TGGTGAATGGAATCTCTCTACGTGGGGCTCGAGAGCCATCTGGCTTGGATATCCA 472
DB 314 TGGTGAATGGAATCTCTCTACGTGGGGCTCGAGAGCCATCTGGCTTGGATATCCA 373
QY 473 GGATCCAGGGGTCCCGAGGCTAAAGAACATGATACCGTGGCCAGGAGTGAAGAGAGAG 532
DB 374 GGATCCAGGGGTCCCGAGGCTAAAGAACATGATACCGTGGCCAGGAGTGAAGAGAGAG 433
QY 533 GAGTGAATGTCCTTTAAGAGAGAGCAATGAGACACAGTGTTCATCTTCACTTCCGTGT 592
DB 434 GAGTGAATGTCCTTTAAGAGAGAGCAATGAGACACAGTGTTCATCTTCACTTCCGTGT 493
QY 593 CTTGTTTCTTACAAATGTCACTTCTACACCTCTGGGAGGCTTCCGCTTCCAGCCCTGC 652
DB 494 CTTGTTTCTTACAAATGTCACTTCTTACACCTCTGGGAGGCTTCCGCTTCCAGCCCTGC 553
QY 653 TTGTACCTTCAATGAATCTCAAGATTCCTACCTGTGGTGGCCATCTCGAGAGCAAGTCTAT 712
DB 554 TTGTACCTTCAATGAATCTCAAGATTCCTACCTGTGGTGGCCATCTCGAGAGCAAGTCTAT 613
QY 713 GGAGGGAAGAGGCAAGGCCCTTTCACCCCGCTCAAGAGTACCGCTGTCTTGGTGA 772
DB 614 GGAGGGAAGAGGCAAGGCCCTTTCACCCCGCTCAAGAGTACCGCTGTCTTGGTGA 673
QY 773 TGGGATGCTCTATTCTTGGTACTATGAACAACTTCTTCCGGGAGTGAAGCCATCTCTGATCG 832
DB 674 TGGGATGCTCTATTCTTGGTACTATGAACAACTTCTTCCGGGAGTGAAGCCATCTCTGATCG 733

QY 833 CACACTGGGATCCAGGCTGTCTCAAGACCCGACAACTTCTCCGCTGGCTGTCATATGA 892
Db 734 CACACTGGGATCCAGGCTGTCTCAAGACCCGACAACTTCTCCGCTGGCTGTCATATGA 793
QY 893 CGCTCTCTTTGTGGAGCCATCCCTTCGAGCCAGGTCGTCTACTTCTTCTTCGAGGAGAC 952
Db 794 CGCTCTCTTTGTGGAGCCATCCCTTCGAGCCAGGTCGTCTACTTCTTCTTCGAGGAGAC 853
QY 953 AGCCAGGAGTTGACTTCTTTGAGAGCTTCCACATCGCGGTGGCTAGAGTCTGCAA 1012
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QY 1013 GAATGAGTGGGGCGGCGAAGAGCTGTGCGAGAGAGTGCACACCTTCTGAAAGGCCCA 1072
Db 914 GAATGAGTGGGGCGGCGAAGAGTGTGCGAGAGAGTGCACACCTTCTGAAAGGCCCA 973
QY 1073 GCTGCTCTGCAACCCAGCGGGGAGCTGCCCTTCAACGTCATCCGCGACCGGTCTGTCT 1132
Db 974 GCTGCTCTGCAACCCAGCGGGGAGCTGCCCTTCAACGTCATCCGCGACCGGTCTGTCT 1033
QY 1133 CCCCAGGATTTCCACAGCTCCCACTCCACATCTACGAGTCTTCCACTCCAGTGGCAGGT 1192
Db 1034 CCCCAGGATTTCCACAGCTCCCACTCCACATCTACGAGTCTTCCACTCCAGTGGCAGGT 1093
QY 1193 TGGCGGACACAGGAGCTCTGGGTTTGTGCTTCTCTCTTGGACATTTGAACTGTCTT 1252
Db 1094 TGGCGGACACAGGAGCTCTGGGTTTGTGCTTCTCTCTTGGACATTTGAACTGTCTT 1153
QY 1253 TAAGGGGAAATACAAAGTTGACAAAGAACTTACGCTGGACTACTTATAGGGGCC 1312
Db 1154 TAAGGGGAAATACAAAGTTGACAAAGAACTTACGCTGGACTACTTATAGGGGCC 1213
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QY 1373 CTTCAATGAGACCAATTTCTGATGAGTATGACAGTGGTGGGACCGCCCTGTGTTGAA 1432
Db 1274 CTTCAATGAGACCAATTTCTGATGAGTATGACAGTGGTGGGACCGCCCTGTGTTGAA 1333
QY 1433 ATCTGGCGTGAGTATACACGGCTTGAGTGGAGACAGCCAGGGCCCTTGATGGGACAG 1492
Db 1334 ATCTGGCGTGAGTATACACGGCTTGAGTGGAGACAGCCAGGGCCCTTGATGGGACAG 1393
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Db 1394 CCACTTCTCATGTGAGTGGGAAACCAACAGGCTCGCTCCACAGGCTGTGTAAAGTGG 1453
QY 1553 GGACAGCAGTGTCTATCTGGTGGAGAGATTCAGTGTCTTCCCTGACCCCTGAACTGTTCG 1612
Db 1454 GGACAGCAGTGTCTATCTGGTGGAGAGATTCAGTGTCTTCCCTGACCCCTGAACTGTTCG 1513
QY 1613 CAACTGAGCTGGGCCCCCAACCGAGGTGAGTGTGTTGATGCTTCTCAGAGGTGTCTG 1672
Db 1514 CAACTGAGCTGGGCCCCCAACCGAGGTGAGTGTGTTGATGCTTCTCAGAGGTGTCTG 1573
QY 1673 GAGGCTGCCCGAGCCAACTGTAGTGTCTATGAGAGCTGTGTGAGCTGTGTCTTGGCCG 1732
Db 1574 GAGGCTGCCCGAGCCAACTGTAGTGTCTATGAGAGCTGTGTGAGCTGTGTCTTGGCCG 1633
QY 1733 GGACCCCCCATGTGCTGGGACCTGTAGTGTCCGGAACCTGTGTCCTCTGTCTGCCCCCAA 1792
Db 1634 GGACCCCCCATGTGCTGGGACCTGTAGTGTCCGGAACCTGTGTCCTCTGTCTGCCCCCAA 1693
QY 1793 CTTGAATCTCTGGAAGCAGGACATGAGCGGGGAAACCCAGAGTGGGCATGTGCCAGTGG 1852
Db 1694 CTTGAATCTCTGGAAGCAGGACATGAGCGGGGAAACCCAGAGTGGGCATGTGCCAGTGG 1753
QY 1853 CCCCATGAGCAGGAGCTTGGCTTCAAGCGGCCCGGCAATCATTTAAAGTCTCTGGC 1912
Db 1754 CCCCATGAGCAGGAGCTTGGCTTCAAGCGGCCCGGCAATCATTTAAAGTCTCTGGC 1813
QY 1913 TGTCCCTAACTCCATCTCTGGAGCTCCCTCGCCCCACCTGTGAGCTTGGCCCTCTTATTA 1972

Db 1814 TGTCCCAACTCCATCTCGAGCTCCCTGCCCCCACCCTGTGAGCCCTTGGCCTCTTATTA 1873
QY 1973 TTGAGTCTATGGCCAGCAGCAGTCCAGAGGCTCTTCCACTGTCTACAAATGGCTCCCT 2032
Db 1874 TTGAGTCTATGGCCAGCAGCAGTCCAGAGGCTCTTCCACTGTCTACAAATGGCTCCCT 1933
QY 2033 CTTGCTGATAGTGCAGGATGGGTTGGGGTCTCTACAGTGTCTGGGCAACTGAGATGG 2092
Db 1934 CTTGCTGATAGTGCAGGATGGGTTGGGGTCTCTACAGTGTCTGGGCAACTGAGATGG 1993
QY 2093 CTTTTCATACCTCTGTATCTCTACTG3GTGGACAGCAGGACAGACCCCTGGCCCTGGA 2152
Db 1994 CTTTTCATACCTCTGTATCTCTACTG3GTGGACAGCAGGACAGACCCCTGGCCCTGGA 2053
QY 2153 TCCTGMACTGACAGCATCCCGGGGAGCATGTGAAGTCCCGTTGACAGGGTCACTGG 2212
Db 2054 TCCTGMACTGACAGCATCCCGGGGAGCATGTGAAGTCCCGTTGACAGGGTCACTGG 2113
QY 2213 TGGGGCCCGCTGGCTGCCAGCAGTCTCTACTG3CCCCACCTTTGTCACTGTCACTGCT 2272
Db 2114 TGGGGCCCGCTGGCTGCCAGCAGTCTCTACTG3CCCCACCTTTGTCACTGTCACTGCT 2173
QY 2273 CTTTTCCTTACTGTCTTTCAGGAGCCCTCATCTCTG3GCCCTCCCATTTGAGAGCACT 2332
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QY 2333 CCGGGCTCGGGCCAAAGTTTCAGGGCTGTGAGACCTCTG3CCCTGGGGAGAGGCCCTTT 2392
Db 2234 CCGGGCTCGGGCCAAAGTTTCAGGGCTGTGAGACCTCTG3CCCTGGGGAGAGGCCCTTT 2293
QY 2393 AAGCAGAGAGCAACACTCTCCAGTCTCCCAAGGATGAGGACCTTCCAGTGTATGGA 2452
Db 2294 AAGCAGAGAGCAACACTCTCCAGTCTCCCAAGGATGAGGACCTTCCAGTGTATGGA 2353
QY 2453 CGCTCAACAACTGCTCTAGGCACTGAGTGTAACTCTAG3CAAG3CCGGGGCTG 2512
Db 2354 CGCTCAACAACTGCTCTAGGCACTGAGTGTAACTCTAG3CAAG3CCGGGGCTG 2413
QY 2513 CGGTGAGGCACTCGCCCATGCTGGCGGCGCCCAAGCAGACGCTTCTAGATGAC 2572
Db 2414 CGGTGAGGCACTCGCCCATGCTGGCGGCGCCCAAGCAGACGCTTCTAGATGAC 2473
QY 2573 AGCAGCACAAGAGACCACTTCTCCCTGAGAGAGCTTCTGTACTCTG3CATCACTGA 2632
Db 2474 AGCAGCACAAGAGACCACTTCTCTCTCCCTGAGAGAGCTTCTGTACTCTG3CATCACTGA 2533
QY 2633 TGACACTGAGGAGTGTGACAGAGTCTG3CTCCCTTATGGAGTCCCTTCTACCAA 2692
Db 2534 TGACACTGAGGAGTGTGACAGAGTCTG3CTCCCTTATGGAGTCCCTTCTACCAA 2593
QY 2693 GCACATGAGCTCTCTAAACAGGGTGGGGCTACCCCCAGACCTGTCTTACATGATATG 2752
Db 2594 GCACATGAGCTCTCTAAACAGGGTGGGGCTACCCCCAGACCTGTCTTACATGATATG 2653
QY 2753 AAGAACTCTGGAGAGTCTTTCAGTGTGGCCATTTCCAGGAGCCCTCCAGAAAACAGTGG 2812
Db 2654 AAGAACTCTGGAGAGTCTTTCAGTGTGGCCATTTCCAGGAGCCCTCCAGAAAACAGTGG 2713
QY 2813 TTTTCAGAGACCTTAAACAACTGCTGTCCAGGACCTTATGTAATGAAACACCAACA 2872
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Db 2774 TCTAAACATATATGCTAAACATG3CATCTCTGGAAAACCTCACTCTGAGTGTGGCTTT 2833
QY 2933 GGACACCACTCTCCCTTCTCCAGGAGTCTG3CAGGAGTCTGCTCCCTCTCTGCTTCCCTT 2992
Db 2834 GGACACCACTCTCCCTTCTCCAGGAGTCTG3CAGGAGTCTGCTCCCTCTCTGCTTCCCTT 2893
QY 2993 ACCAGTCTG3CAGGAGTCTCCCTCCAGGAGTCTTCCCTGAACTGTGACCACTTCTTCT 3052

QY	1553	GGACAGCAGTGTCTCATCTGTGTGAAGAGATTACAGCTGTTCCCTGACCCCTGAACCTGTGTCG	1612
Db	1454	GGACAGCAGTGTCTCATCTGTGTGAAGAGATTACAGCTGTTCCCTGACCCCTGAACCTGTGTCG	1513
QY	1613	CAACCTCAGCTGSCCCCCCAACCCAGGGGTGCAGTGTGTTGTAGGCTTCTCAGAGAGTGTCTG	1672
Db	1514	CAACCTCAGCTGSCCCCCCAACCCAGGGGTGCAGTGTGTTGTAGGCTTCTCAGAGAGTGTCTG	1573
QY	1673	GAGGGTCCCCAGCCAACTGTATGTCTATGAGAGCTGTGTGGACTGTGTCTGTGCCCCG	1732
Db	1574	GAGGGTCCCCAGCCAACTGTATGTCTATGAGAGCTGTGTGGACTGTGTCTGTGCCCCG	1633
QY	1733	GGACCCCACTGTGCTTGGGACCTGAGTCCCGAACCTGTGTGCTCCTGTCTGTCTGCCCCAA	1792
Db	1634	GGACCCCACTGTGCTTGGGACCTGAGTCCCGAACCTGTGTGCTCCTGTCTGTCTGCCCCAA	1693
QY	1793	CCTGAACTCCTTGGGAAGCAGGACATGGAGCGGGGGAACCCAGAGTGGGCATGTGTCCAGTGG	1852
Db	1694	CCTGAACTCCTTGGGAAGCAGGACATGGAGCGGGGGAACCCAGAGTGGGCATGTGTCCAGTGG	1753
QY	1853	CCCATGAGCAGGAGCCTTGGGCTCAGAGCGCCCGCAATCATTAAGAAGTGTCTGTGCG	1912
Db	1754	CCCATGAGCAGGAGCCTTGGGCTCAGAGCGCCCGCAATCATTAAGAAGTGTCTGTGCG	1813
QY	1913	TGTCCTTAACCTCACTCTGGAGCTCCCTGTGCCCCCACTGTGCAGCCTTGGCCTCTTATTA	1972
Db	1814	TGTCCTTAACCTCACTCTGGAGCTCCCTGTGCCCCCACTGTGCAGCCTTGGCCTCTTATTA	1873
QY	1973	TTGGAGTCTAGGCCCGACAGCAGTCCAGAGAGCCTCTTCCACTGTCTACAAATGGCTCCCT	2032
Db	1874	TTGGAGTCTAGGCCCGACAGCAGTCCAGAGAGCCTCTTCCACTGTCTACAAATGGCTCCCT	1933
QY	2033	CTTGCTGATAGTGCAGGATGGAGTTGGGGGTCTTACCAAGTGTCTGGGCAACTGAGAAATGG	2092
Db	1934	CTTGCTGATAGTGCAGGATGGAGTTGGGGGTCTTACCAAGTGTCTGGGCAACTGAGAAATGG	1993
QY	2093	CTTTTTCATACCTTGTGTATCTCTACTGTGGTGGACAGCAGGACAGACCTGTGSCCTTGGGA	2152
Db	1994	CTTTTTCATACCTTGTGTATCTCTACTGTGGTGGACAGCAGGACAGACCTGTGSCCTTGGGA	2053
QY	2153	TCCTGAACTGGCAGGCATCCCCCGGAGCATGTGAAGGTCCCGTTGACCAAGGGTCAAGTGG	2212
Db	2054	TCCTGAACTGGCAGGCATCCCCCGGAGCATGTGAAGGTCCCGTTGACCAAGGGTCAAGTGG	2113
QY	2213	TGGGGCGCCCTGTGCTGCCAGCAGTCTCTACTGTGCCCACTTTTGTCTACTGTCTGTCTCT	2272
Db	2114	TGGGGCGCCCTGTGCTGCCAGCAGTCTCTACTGTGCCCACTTTTGTCTACTGTCTGTCTCT	2173
QY	2273	CTTTTGCCTTAGTGTCTTTCAGGAGCCCTCATCATCTGTGTGGCTTCCCATTTGAGAGCACT	2332
Db	2174	CTTTTGCCTTAGTGTCTTTCAGGAGCCCTCATCATCTGTGTGGCTTCCCATTTGAGAGCACT	2233
QY	2333	CCGGGCTCGGGGCAAGGTTTACGGGCTGTGAGACCTGTGCCCTGTGGGAGAGGGCCCCGTT	2392
Db	2234	CCGGGCTCGGGGCAAGGTTTACGGGCTGTGAGACCTGTGCCCTGTGGGAGAGGGCCCCGTT	2293
QY	2393	AAGCAGAGAGCAACACCTTCCAGTCTCCCAAGGAATGACAGGACCTCTGTGAGTGATGTGGA	2452
Db	2294	AAGCAGAGAGCAACACCTTCCAGTCTCCCAAGGAATGACAGGACCTCTGTGAGTGATGTGGA	2353
QY	2453	CGCTGACAAACCTGCTTAGGCACTGAGGTTAGCTTTAACTCTTAGGCAAGGCGGGGCTG	2512
Db	2354	CGCTGACAAACCTGCTTAGGCACTGAGGTTAGCTTTAACTCTTAGGCAAGGCGGGGCTG	2413
QY	2513	CGGTGCAGGCACCTGTGGCCATCTGTGGTGGGGGCCCAAGCACACCCCTGACTAGGATGAC	2572
Db	2414	CGGTGCAGGCACCTGTGGCCATCTGTGGTGGGGGCCCAAGCACACCCCTGACTAGGATGAC	2473
QY	2573	AGCAGCAAAAAGACCACTTTCTCCCTGTAGAGAGGCTTCTGTACTCTGTGCATCACTGA	2632
Db	2474	AGCAGCAAAAAGACCACTTTCTCCCTGTAGAGAGGCTTCTGTACTCTGTGCATCACTGA	2533

RESULT 12

RESULI 12
US-10-012-121A-276
: Sequence 276. Application US/10012121A

: GENERAL INFORMATION:

APPLICANT: Baker, Kevin P.

APPLICANT: BAKER, KEVIN P.
APPLICANT: Botstein David

APPLICANT: Botstein, David

; APPLICANT: Desnoyers, Luc

APPLICANT: Eaton, Dan l.

; APPLICANT: Ferrara, Napoli

; APPLICANT: Fong, Sherman

APPLICANT: Gao, Wei-Qiang

APPLICANT: Goddard, Audrey

APPLICANT: Godowski, Paul J.

APPLICANT: GRIMALDI, CHRISTOPHER

APPLICANT: GRIMALDI, CHRISTOPHER
APPLICANT: GURNEY, AUGUSTINE

APPLICANT: Gurney, Austin
APPLICANT: Hillen
APPLICANT: Koppert

APPLICANT: Hillan, Kenneth J.

APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

FILE OF INVENTION: ACIDS encoding the 3a
FILE REFERENCE: P2830P1C20

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; FILE REFERENCE: P2830PIC20
; CURRENT APPLICATION NUMBER: IIS/10/012 121A

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; CURRENT APPLICATION NUMBER: US/10/012,121A
; CURRENT FILING DATE: 2001 12 07

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2001-12-07

; Prior Application removed

; NUMBER OF SEQ ID NOS: 477

; SEQ ID NO 276

; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-10-012-121A-276

Query Match 87.3%; Score 3060.8; DB 15; Length 3143;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 3062; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY	173	AGAGCTCCCTGGTGACAGTCTGTGGCTGAGCATGGCCCTCCAGAGCCCTGGGGCTGGAGCC	232
DB	74	AGAGCTCCCTGGTGACAGTCTGTGGCTGAGCATGGCCCTCCAGAGCCCTGGGGCTGGAGCC	133
QY	233	CTGGAGCCTCTCTGGGCTTTTCTCTTCAAATGCTTCAAGTCTGCTGCTGCTCGAGACGAC	292
DB	134	CTGGAGCCTCTCTGGGCTTTTCTCTTCAAATGCTTCAAGTCTGCTGCTGCTCGAGACGAC	193
QY	293	CGCGGGGGAGGGCGGCGAGGGGCCATGGCCAGGGTCAGATACTATGCAAGGGGATGAACG	352
DB	194	CGCGGGGGAGGGCGGCGAGGGGCCATGGCCAGGGTCAGATACTATGCAAGGGGATGAACG	253
QY	353	TAGGGCACTTAGCTTTTCCACAGAAAGGGCTCCAGAGTTTGGACACTTCTCTCTGAG	412
DB	254	TAGGGCACTTAGCTTTTCCACAGAAAGGGCTCCAGAGTTTGGACACTTCTCTCTGAG	313
QY	413	TGTTGATGGAAATACTCTTCACTGCTGGGGGCTCGAGAAGCCATTCTGGCCTTGGATATCA	472
DB	314	TGTTGATGGAAATACTCTTCACTGCTGGGGGCTCGAGAAGCCATTCTGGCCTTGGATATCA	373
QY	473	GGATCCAGGGGTCCCAGGGCTAAAGACATGATACCGTGGCGAGCCAGTGACAGAAAAA	532
DB	374	GGATCCAGGGGTCCCAGGGCTAAAGACATGATACCGTGGCGAGCCAGTGACAGAAAAA	433
QY	533	GAGTGAATGTGCCCTTTTAAGAAAGAGGCAATGAGACACAGTGTTCACATTCATCGGT	592
DB	434	GAGTGAATGTGCCCTTTTAAGAAAGAGGCAATGAGACACAGTGTTCACATTCATCGGT	493
QY	593	CCTGGTTCTTCAAGTGTACCCATCTCTACACTGCGGACCTTCGCCTTCAGCCCTCG	652
DB	494	CCTGGTTCTTCAAGTGTACCCATCTCTACACTGCGGACCTTCGCCTTCAGCCCTCG	553
QY	653	TTGTACCTTCATTGAACTTCAAGATTCTTACCTTGTGCCCATCTCGAGAGCAAGTCA	712
DB	554	TTGTACCTTCATTGAACTTCAAGATTCTTACCTTGTGCCCATCTCGAGAGCAAGTCA	613
QY	713	GGAGGAAAGGCCAAGCCCTTTGACCCGCTTCAAGCATACGGCTTACAGCATACGGCTGT	772
DB	614	GGAGGAAAGGCCAAGCCCTTTGACCCGCTTCAAGCATACGGCTTACAGCATACGGCTGT	673
QY	773	TGGGATGCTCTATTCTGGTACTATGAACAATCTTCTGGGCAGTGAGCCCATTCGTAG	832
DB	674	TGGGATGCTCTATTCTGGTACTATGAACAATCTTCTGGGCAGTGAGCCCATTCGTAG	733
QY	833	CACACTGGATCCAGCCTGTCTCAAGACCGACAATCTCTCGCTGGCTGCATCATGA	892
DB	734	CACACTGGATCCAGCCTGTCTCAAGACCGACAATCTCTCGCTGGCTGCATCATGA	793
QY	893	CGCTCTCTTGTGGACGCATTCCTTTCGACCCAGGTGCTGTACTTCTTCTTCGAGAGAC	952
DB	794	CGCTCTCTTGTGGACGCATTCCTTTCGACCCAGGTGCTGTACTTCTTCTTCGAGAGAC	853
QY	953	AGCCAGCGAGTTTGCATTTCTTTGAGAGGCTCCACACATCGGGGTGGCTAGAGTCTGCA	1012
DB	854	AGCCAGCGAGTTTGCATTTCTTTGAGAGGCTCCACACATCGGGGTGGCTAGAGTCTGCA	913
QY	1013	GAATGAATGGCGCGGAAAAAGCTGCTGCAGAAAGATGGACCACTTCTTGAAGGCCCA	1072
DB	914	GAATGAATGGCGCGGAAAAAGCTGCTGCAGAAAGATGGACCACTTCTTGAAGGCCCA	973
QY	1073	GCTGCTCTGCACCCAGCCGGGCGAGCTGCCCTTCAAAGTCAATCGGCCACGGGCTCTGCT	1132
DB	974	GCTGCTCTGCACCCAGCCGGGCGAGCTGCCCTTCAAAGTCAATCGGCCACGGGCTCTGCT	1033
QY	1133	CCCCGCGAATCTCCACAGCTTCCCCACATCTAAGAGTCTTCACTTCCAGTGGCAGGT	1192

Db 2114 TGGGGCCGCTGGCTGCCAGAGTCTCTAGTGGCCCACTTTGTCACTGTCACTGTCT 2173
QY 2273 CTTTGCCCTTAGTGTCTTTCAGAGCCCTCATCATCTCTGTGGCCCTCCCATGTAGAGACT 2332
Db 2174 CTTTGCCCTTAGTGTCTTTCAGAGCCCTCATCATCTCTGTGGCCCTCCCATGTAGAGACT 2233
QY 2333 CCGGCTCGGGCAAGGTTTCAGGGCTGTGAGACCTCTGGCCCTCGGGAGAGGCCCCGTT 2392
Db 2234 CCGGCTCGGGCAAGGTTTCAGGGCTGTGAGACCTCTGGCCCTCGGGAGAGGCCCCGTT 2293
QY 2393 AGCAGAGAGCAACACTCCAGTCTCCCAAGGATGAGGACCTCTGCGAGTGTATGGA 2452
Db 2294 AGCAGAGAGCAACACTCCAGTCTCCCAAGGATGAGGACCTCTGCGAGTGTATGGA 2353
QY 2453 CGCTGACCAACTCCCTAGGCACTGAGGTAGCTTAACTCTAGGCAAGGCCCCGCTG 2512
Db 2354 CGCTGACCAACTCCCTAGGCACTGAGGTAGCTTAACTCTAGGCAAGGCCCCGCTG 2413
QY 2513 CGGTGAGGCACTGGCCATGCTGGCTGGGCGGCCCAAGCAAGCCCTGACTAGGATGAC 2572
Db 2414 CGGTGAGGCACTGGCCATGCTGGCTGGGCGGCCCAAGCAAGCCCTGACTAGGATGAC 2473
QY 2573 AGCAGCAAAAGACACACTTCTCCCTGAGAGGAGCTTCTGTACTCTGCATCACTGA 2632
Db 2474 AGCAGCAAAAGACACACTTCTCCCTGAGAGGAGCTTCTGTACTCTGCATCACTGA 2533
QY 2633 TGACACTCAGCAGGGTGTATGACAGAGCTGTGCTTCCCTATGGGACTTCCCTTCAACAA 2692
Db 2534 TGACACTCAGCAGGGTGTATGACAGAGCTGTGCTTCCCTATGGGACTTCCCTTCAACAA 2593
QY 2693 GCACATGAGCTCTTAACAGAGGTGGGCTACCCAGAGCTGTCTTACACTGATATTG 2752
Db 2594 GCACATGAGCTCTTAACAGAGGTGGGCTACCCAGAGCTGTCTTACACTGATATTG 2653
QY 2753 AAGAACTGGAGAGGATCTTCACTTGTGGCCATTCAGGAGACCTCCAGAAACACAGTG 2812
Db 2654 AAGAACTGGAGAGGATCTTCACTTGTGGCCATTCAGGAGACCTCCAGAAACACAGTG 2713
QY 2813 TTTCAGAGAGCCCTAAAGACCTGCTGTCAGGAGCCCTATGATGATGACACCAACA 2872
Db 2714 TTTCAGAGAGCCCTAAAGACCTGCTGTCAGGAGCCCTATGATGATGACACCAACA 2773
QY 2873 TCTAAACATCATATGCTTAACATGCCACTCTCTGGAACCTCCACTCTGAGGTCGCGCTTT 2932
Db 2774 TCTAAACATCATATGCTTAACATGCCACTCTCTGGAACCTCCACTCTGAGTGGCGCTTT 2833
QY 2933 GGAACCAACACTCCCTTCTCCAGGTCATGAGGAGTCTGCTCCCTCTGCTTCCCTT 2992
Db 2834 GGAACCAACACTCCCTTCTCCAGGTCATGAGGAGTCTGCTCCCTCTGCTTCCCTT 2893
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Db 2894 ACCAGTCTGACCGCTGACTCCAGGAGGTCCTTCCCTGAGTCTGACCACTTCTTCT 2953
QY 3053 TGCTTCACTGGGAGAGTCTGATTCCTTCTGCGGTCATGAGGAGTCTGCTCCCTGCTTCT 3112
Db 2954 TGCTTCACTGGGAGAGTCTGATTCCTTCTGCGGTCATGAGGAGTCTGCTCCCTGCTTCT 3013
QY 3113 AGCTTCTTCACTCTTACCTAGTCTGACCCCTTCACTCTCCCTCTCCCTTCTTCTT 3172
Db 3014 AGCTTCTTCACTCTTACCTAGTCTGACCCCTTCACTCTCCCTCTCCCTTCTTCTT 3073
QY 3173 GTTTGGGATTCAGAAACTGCTTGTGAGAGTCTGTTTATTTTATTAATAATAAGG 3232
Db 3074 GTTTGGGATTCAGAAACTGCTTGTGAGAGTCTGTTTATTTTATTAATAATAAGG 3133
QY 3233 CTTA 3236
Db 3134 CTTA 3137

RESULT 13

US-10-006-116A-276

; Sequence 276, Application US/10006116A
; Publication No. US20030082826A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan I.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2830P1C15
; CURRENT APPLICATION NUMBER: US/10/006,116A
; CURRENT FILING DATE: 2001-12-16
; PRIOR APPLICATION NUMBER: 60/098716
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; PRIOR FILING DATE: 1998-09-16
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; PRIOR APPLICATION NUMBER: 60/105882
; PRIOR FILING DATE: 1998-10-27
; PRIOR APPLICATION NUMBER: 60/106023
; PRIOR FILING DATE: 1998-10-28

Query Match      87.3%; Score 3060.8; DB 15; Length 3143;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 3062; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 173 AGAGTCCCTGGTGACAGTCTGTGGCTGAGCATGGCCCTCCAGCCCTCCAGCCCTGGGCTGACCC 232
Db 74 AGAGTCCCTGGTGACAGTCTGTGGCTGAGCATGGCCCTCCAGCCCTCCAGCCCTGGGCTGACCC 133
Qy 233 CTGGAGCCTCCCTGGGGCTTTTCTCTTCCAACTGCTTCAAGTCTGCTGCCGACGACGAC 292
Db 134 CTGGAGCCTCCCTGGGGCTTTTCTCTTCCAACTGCTTCAAGTCTGCTGCCGACGACGAC 193
Qy 293 CGCGGGGGAGGCGGCGAGGCGCCCATGCCAGGGTTCAGATATGACAGGGATGAACG 352
Db 194 CGCGGGGGAGGCGGCGAGGCGCCCATGCCAGGGTTCAGATATGACAGGGATGAACG 253
Qy 353 TAGGGCATTAGCTTCTTCCACAGAGGCGCTCCAGGATTTTGACATCTCTCTCTGAG 412
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Db	254	TAGGGCACTTAGCTTCTTCCACAGAGGGGCTCCAGATTTTTCACACTCTGCTCCTGAG	313
Qy	413	TGGTGAATGGAATACTCTCTACGTGGGGGCTCGAAGAGCAATTCCTGGCCCTTGGATATCCA	472
Db	314	TGGTGAATGGAATACTCTCTACGTGGGGGCTCGAAGAGCAATTCCTGGCCCTTGGATATCCA	373
Qy	473	GGATCCAGGGGTCCCAAGGCTTAAAGAACATGATACCGTGGCCAGGCAAGTGCACAGAAATAA	532
Db	374	GGATCCAGGGGTCCCAAGGCTTAAAGAACATGATACCGTGGCCAGGCAAGTGCACAGAAATAA	433
Qy	533	GAGTGAATGTCCCTTTAAGAAAGAGCAATGAGACACAGTGTTCAACTTCATCCGTGT	592
Db	434	GAGTGAATGTCCCTTTAAGAAAGAGCAATGAGACACAGTGTTCAACTTCATCCGTGT	493
Qy	593	CCTGGTTCCTTACAAATGTACCCATCTCTACACCTGGGACACCTTCGCCCTTCAGCCCTGC	652
Db	494	CCTGGTTCCTTACAAATGTACCCATCTCTACACCTGGGACACCTTCGCCCTTCAGCCCTGC	553
Qy	653	TTGTACCTTCAATGAACCTTAAAGATTCCTACCTTTGGCCATCTCTGGAGCAAGGTAT	712
Db	554	TTGTACCTTCAATGAACCTTAAAGATTCCTACCTTTGGCCATCTCTGGAGCAAGGTAT	613
Qy	713	GGAGGAAAGGCGCAAGCCCTTTGACCCCGCTCAAGACATACGGCTGTCTTGGTGA	772
Db	614	GGAGGAAAGGCGCAAGCCCTTTGACCCCGCTCAAGACATACGGCTGTCTTGGTGA	673
Qy	773	TGGATGCTCTATTCTGGTACTATGAACAACTTCTGGGAGTGAGCCCATCTCTGATGCG	832
Db	674	TGGATGCTCTATTCTGGTACTATGAACAACTTCTGGGAGTGAGCCCATCTCTGATGCG	733
Qy	833	CACACTGGATCCAGGCTGTCTCAAGACCGACAACTTCTCGCTGGCTGGTGCATATGA	892
Db	734	CACACTGGATCCAGGCTGTCTCAAGACCGACAACTTCTCGCTGGCTGGTGCATATGA	793
Qy	893	CGCTCTCTTTGTGGCAGCCATCCCTTCGACCAGGTCTCTACTTCTTCTTCGAGGAGAC	952
Db	794	CGCTCTCTTTGTGGCAGCCATCCCTTCGACCAGGTCTCTACTTCTTCTTCGAGGAGAC	853
Qy	953	AGCCAGCAGATTCATCTCTTTGAGAGCTCCACACATCGGGTGGCTAGTCTGCAA	1012
Db	854	AGCCAGCAGATTCATCTCTTTGAGAGCTCCACACATCGGGTGGCTAGTCTGCAA	913
Qy	1013	GAATGACGTGGCGCGGAGAAAGCTGTGTCAGAAAGTGGACCACTTCTCTGAGGCCCCA	1072
Db	914	GAAATGACGTGGCGCGGAGAAAGCTGTGTCAGAAAGTGGACCACTTCTCTGAGGCCCCA	973
Qy	1073	GCTGCTCTGCAACCGCGGGAGCTGCTTCAAGTCTCAAGTCTCGCCACGCGGTCTGCT	1132
Db	974	GCTGCTCTGCAACCGCGGGAGCTGCTTCAAGTCTCAAGTCTCGCCACGCGGTCTGCT	1033
Qy	1133	CCCCGCCGATTCCTCCACAGCTCCCCCATCTACGCACTTTCACCTCCGAGTGGCAGGT	1192
Db	1034	CCCCGCCGATTCCTCCACAGCTCCCCCATCTACGCACTTTCACCTCCGAGTGGCAGGT	1093
Qy	1193	TGGCGGGAACAGGAGCTCTGGGTTTGGCTTCTCTCTCTTGGACATGAACTGTCTT	1252
Db	1094	TGGCGGGAACAGGAGCTCTGGGTTTGGCTTCTCTCTCTTGGACATGAACTGTCTT	1153
Qy	1253	TAAAGGGAATACAAAGAGTTGAACAAAGAACTTCACGCTGGACTACTTATAGGGGCC	1312
Db	1154	TAAAGGGAATACAAAGAGTTGAACAAAGAACTTCACGCTGGACTACTTATAGGGGCC	1213
Qy	1313	TGAGACCAACCCCGCGCAGGAGTTGCTCAGTGGGCCCTCTCTGATATAGGCCCTGAC	1372
Db	1214	TGAGACCAACCCCGCGCAGGAGTTGCTCAGTGGGCCCTCTCTGATATAGGCCCTGAC	1273
Qy	1373	CTTCATGAGGACCAATTCCTGATGATGAGCAAGTGTGGGAGCGCCCTCTGCTGTGAA	1432
Db	1274	CTTCATGAGGACCAATTCCTGATGATGAGCAAGTGTGGGAGCGCCCTCTGCTGTGAA	1333
Qy	1433	ATCTGGCGTGGAGTATACCGGCTTGCAGTGGAGACAGCCAGGCGCTTGTATGGGCAAG	1492
Db	1334	ATCTGGCGTGGAGTATACCGGCTTGCAGTGGAGACAGCCAGGCGCTTGTATGGGCAAG	1393

Qy	1493	CCATCTTCTCATGTACTTGGGAAACCAACACAGGGTCCCTCCACAGGCTGTGTAAGTGG	1552
Db	1394	CCATCTTCTCATGTACTTGGGAAACCAACACAGGGTCCCTCCACAGGCTGTGTAAGTGG	1453
Qy	1553	GGACAGAGTGTCTCATCTGTGTGGAGAGATTCACTGTTCCTCAACCTGAACTGTTCG	1612
Db	1454	GGACAGAGTGTCTCATCTGTGTGGAGAGATTCACTGTTCCTCAACCTGAACTGTTCG	1513
Qy	1613	CAACCTGCAGCTGGCCCCCACCAGGGTGCAGTGTTCCTAGGCTTCTCAGAGGTGTCTG	1672
Db	1514	CAACCTGCAGCTGGCCCCCACCAGGGTGCAGTGTTCCTAGGCTTCTCAGAGGTGTCTG	1573
Qy	1673	GAGGCTGGCCCCGAGCCAACTGTGTATAGAGCTGTGTGCACTGTGTCTTTCGCTG	1732
Db	1574	GAGGCTGGCCCCGAGCCAACTGTGTATAGAGCTGTGTGCACTGTGTCTTTCGCTG	1633
Qy	1733	GGACCCCACTGTGCTGGGACCTGAGTCCCGAACCTGTTCCTCTGCTGCTGCCCCAA	1792
Db	1634	GGACCCCACTGTGCTGGGACCTGAGTCCCGAACCTGTTCCTCTGCTGCTGCCCCAA	1693
Qy	1793	CCTGAACCTCTGGAGCAGGACATGAGCGGGGAAACCCAGAGTGGGCATGTGCACTGG	1852
Db	1694	CCTGAACCTCTGGAGCAGGACATGAGCGGGGAAACCCAGAGTGGGCATGTGCACTGG	1753
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Db	1754	CCCCATGAGCAGGAGCTTTCGGCTCAGAGCGCCCGCCAAATCATTAAGAGTCTCTGGC	1813
Qy	1913	TGTCCTTAACCTCACTCTGGAGCTCCCTGCCCCCACCTGTGAGCTTGGCTCTTTATTA	1972
Db	1814	TGTCCTTAACCTCACTCTGGAGCTCCCTGCCCCCACCTGTGAGCTTGGCTCTTTATTA	1873
Qy	1973	TTGGAGTATGAGCCAGCAGAGCTCCAGAGAGCTCTTCCACTGTCTCAATGAGTCTCCT	2032
Db	1874	TTGGAGTATGAGCCAGCAGAGCTCCAGAGAGCTCTTCCACTGTCTCAATGAGTCTCCT	1933
Qy	2033	CTTGTCTGATGAGTGGAGTGGAGTTGGGGTCTCTACCAAGTGTGGGCAACTGAGAAATGG	2092
Db	1934	CTTGTCTGATGAGTGGAGTGGAGTTGGGGTCTCTACCAAGTGTGGGCAACTGAGAAATGG	1993
Qy	2093	CTTTTCTATACCTGTGATCTCTCTACTGGGTGAGCAGCAGGACCAAGCTCTGGCCCTGGA	2152
Db	1994	CTTTTCTATACCTGTGATCTCTCTACTGGGTGAGCAGCAGGACCAAGCTCTGGCCCTGGA	2053
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Db	2054	TCTGTAACCTGGCAGGACATCCCGCGGAGCATGTGAAGTCCCGTTGACACAGGTCAGTGG	2113
Qy	2213	TGGGCGCGCTTGGCTGGCCAGCAGTCTCTATCTGGCCCCCATTTTGTCTCATGTCTCT	2272
Db	2114	TGGGCGCGCTTGGCTGGCCAGCAGTCTCTATCTGGCCCCCATTTTGTCTCATGTCTCT	2173
Qy	2273	CTTTGCTTTAGTGTCTTTCAGAGAGCTCTCATCATCTCTGCTGGCTCCCATTTGAGAGCACT	2332
Db	2174	CTTTGCTTTAGTGTCTTTCAGAGAGCTCTCATCATCTCTGCTGGCTCCCATTTGAGAGCACT	2233
Qy	2333	CCGGGCTCGGGCAAGGTTTACGGGTGTGAGACCTCTGCGCCCTGGGGAGAGGCCCGGTT	2392
Db	2234	CCGGGCTCGGGCAAGGTTTACGGGTGTGAGACCTCTGCGCCCTGGGGAGAGGCCCGGTT	2293
Qy	2393	AAGCAGAGAGCAACCTCCAGTCTCCAAAGAAATGACAGGACCTCTGCGAGTGTGGA	2452
Db	2294	AAGCAGAGAGCAACCTCCAGTCTCCAAAGAAATGACAGGACCTCTGCGAGTGTGGA	2353
Qy	2453	CGCTGACAACTGCTAGGCACTGAGTGTAGTCTTAACTCTAGGCAAGGCCCGGGCTG	2512
Db	2354	CGCTGACAACTGCTAGGCACTGAGTGTAGTCTTAACTCTAGGCAAGGCCCGGGCTG	2413
Qy	2513	CGGTGACGACCTTGGCCATGCTGCTGGCGCCCGCCAAAGCAAGCCCTGACTAGATGAC	2572
Db	2414	CGGTGACGACCTTGGCCATGCTGCTGGCGCCCGCCAAAGCAAGCCCTGACTAGATGAC	2473

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Db	2474	AGCAGCA	CAAAAG	CAACCTTTCTCCCTC	GAGAGG	AGCTTCTGCTA	CTCTGCAT	CACTGA	2533	
Qy	2633	TGACACT	CAGCAGG	GTCATG	CACAGC	AGTCTG	CGCTCC	CGCTATGG	AGCTCCCTTCTAC	2692
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Qy	2813	TTTCA	GAGACC	CTTAAAA	AACTG	CTCC	CAGG	ACCTATG	GTAA	2872
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Db	2894	ACGAGT	CGTGG	CACCG	CTGACT	CC	CAG	AGATCT	TCCCTG	2953
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Qy	3113	AGCCTT	CTTCA	CTCCTTTA	CCCTA	GTG	CA	CCCTTCA	CCCTCT	3172
Db	3014	AGCCTT	CTTCA	CTCCTTTA	CCCTA	GTG	CA	CCCTTCA	CCCTCT	3073
Qy	3173	GTCTTT	GGGATTC	AGAAA	ACTG	CTTGT	CAG	AG	CTGTTATTT	3232
Db	3074	GTCTTT	GGGATTC	AGAAA	ACTG	CTTGT	CAG	AG	CTGTTATTT	3133
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773	TGGGATGCTCTATTCTGTGTAATATGAAACAATCTCTGGGAGTGAGGCCCATCTGATGCG	832	TGGGATGCTCTATTCTGTGTAATATGAAACAATCTCTGGGAGTGAGGCCCATCTGATGCG
674	TGGGATGCTCTATTCTGTGTAATATGAAACAATCTCTGGGAGTGAGGCCCATCTGATGCG	733	TGGGATGCTCTATTCTGTGTAATATGAAACAATCTCTGGGAGTGAGGCCCATCTGATGCG
833	CACACTGGGATCCAGCGCTGTCTCAAGACGCAAACTTCTTCGTGGGTGCAATCATGA	892	CACACTGGGATCCAGCGCTGTCTCAAGACGCAAACTTCTTCGTGGGTGCAATCATGA
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893	CGCCTCTCTTTGGCAGCGCATCCCTTCGACCCAGGTGCTACTTCTTCGTGGAGGAGAC	952	CGCCTCTCTTTGGCAGCGCATCCCTTCGACCCAGGTGCTACTTCTTCGTGGAGGAGAC
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953	AGCCAGCAGGTTTGACTTTCTTTGAGAGGCTCCACACATCGCGGTGGCTAGAGTCTGCAA	1012	AGCCAGCAGGTTTGACTTTCTTTGAGAGGCTCCACACATCGCGGTGGCTAGAGTCTGCAA
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1073 GCTGCTGTGACCCAGCGCGGGGAGCTGCCCTTCAAGCTCATCCGCCACGCGGTCTGCT 1132
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Db 3134 CTTA 3137

RESULT 15

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; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

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; PRIOR APPLICATION NUMBER: 60/101915

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; PRIOR APPLICATION NUMBER: 60/101916

; PRIOR FILING DATE: 1998-09-24

; PRIOR APPLICATION NUMBER: 60/102207

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; PRIOR APPLICATION NUMBER: 60/102240

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Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA.*
1: /cgm2_6/ptodata/2/ina/5A COMB.seq.*
2: /cgm2_6/ptodata/2/ina/5B COMB.seq.*
3: /cgm2_6/ptodata/2/ina/6A COMB.seq.*
4: /cgm2_6/ptodata/2/ina/6B COMB.seq.*
5: /cgm2_6/ptodata/2/ina/PCTUS COMB.seq.*
6: /cgm2_6/ptodata/2/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	230	6.6	2433	4	US-09-300-958A-24
2	153.4	4.4	4157	4	US-08-556-422A-1
3	126	3.6	3524	4	US-09-077-940A-3
4	125.4	3.6	3692	4	US-09-077-940A-1
5	102	2.9	2278	4	US-09-976-594-1002
6	98.6	2.8	121	4	US-08-833-381-202
7	98.6	2.8	2790	4	US-08-254-594-5
8	98.6	2.8	3432	4	US-08-254-594-4
9	89.8	2.6	2787	4	US-08-254-594-2
10	89.8	2.6	3195	4	US-08-254-594-1
11	84.2	2.4	4286	4	US-09-976-594-632
12	78.6	2.2	3560	1	US-08-121-713D-59
13	78.6	2.2	3560	1	US-08-835-268-59
14	78.6	2.2	3560	2	US-09-060-692-59
15	78.6	2.2	3560	3	US-08-833-391-59
16	78.6	2.2	3560	4	US-09-060-610-59
17	78.6	2.2	3560	5	PCT-US94-10151A-59
18	78.2	2.2	1923	4	US-09-653-274-12
19	78.2	2.2	3261	4	US-09-653-274-5
20	78.2	2.2	3694	4	US-09-653-274-3
21	69.8	2.0	2670	1	US-08-121-713D-61
22	69.8	2.0	2670	1	US-08-835-268-61
23	69.8	2.0	2670	1	US-09-060-692-61
24	69.8	2.0	2670	3	US-08-833-391-61
25	69.8	2.0	2670	4	US-09-060-610-61
26	69.8	2.0	2670	5	PCT-US94-10151A-61
27	63.8	1.8	2601	1	US-08-121-713D-53

28	63.8	1.8	2601	1	US-08-835-268-53	Sequence 53, Appl
29	63.8	1.8	2601	2	US-09-060-692-53	Sequence 53, Appl
30	63.8	1.8	2601	3	US-08-833-391-53	Sequence 53, Appl
31	63.8	1.8	2601	4	US-09-060-610-53	Sequence 53, Appl
32	63.8	1.8	2601	5	PCT-US94-10151A-53	Sequence 53, Appl
33	62.6	1.8	7218	1	US-08-232-463-14	Sequence 14, Appl
34	62	1.8	2854	1	US-08-121-713D-57	Sequence 57, Appl
35	62	1.8	2854	2	US-08-835-268-57	Sequence 57, Appl
36	62	1.8	2854	3	US-09-060-692-57	Sequence 57, Appl
37	62	1.8	2854	4	US-08-833-391-57	Sequence 57, Appl
38	62	1.8	2854	5	US-09-060-610-57	Sequence 57, Appl
39	62	1.8	2854	5	PCT-US94-10151A-57	Sequence 57, Appl
40	52.6	1.5	2898	4	US-09-308-179B-2	Sequence 2, Appl
41	50.2	1.4	2504	1	US-08-121-713D-63	Sequence 63, Appl
42	50.2	1.4	2504	1	US-08-835-268-63	Sequence 63, Appl
43	50.2	1.4	2504	2	US-09-060-692-63	Sequence 63, Appl
44	50.2	1.4	2504	3	US-08-833-391-63	Sequence 63, Appl
45	50.2	1.4	2504	4	US-09-060-610-63	Sequence 63, Appl

ALIGNMENTS

RESULT 1

US-09-300-958A-24
; Sequence 24, Application US/09300958A
; Patent No. 6495319
; GENERAL INFORMATION:
; APPLICANT: McClelland, Michael
; APPLICANT: Trengle, John
; APPLICANT: Welsh, John
; TITLE OF INVENTION: Reduced Complexity Nucleic Acid Targets and Methods of
; FILE REFERENCE: P-PH 3457
; CURRENT FILING DATE: 1999-04-27
; CURRENT APPLICATION NUMBER: US/09/300,958A
; PRIOR FILING DATE: 1998-04-27
; PRIOR APPLICATION NUMBER: 60/083,331
; PRIOR FILING DATE: 1998-04-27
; PRIOR APPLICATION NUMBER: 60/098,070
; PRIOR FILING DATE: 1998-08-27
; PRIOR APPLICATION NUMBER: 60/118,624
; PRIOR FILING DATE: 1999-02-04
; NUMBER OF SEQ ID NOS: 85
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 24
; LENGTH: 2433
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-300-958A-24

Query Match 6.6%; Score 230; DB 4; Length 2433;
Best Local Similarity 50.2%; Pred. No. 2.4e-53;
Matches 906; Conservative 0; Mismatches 805; Indels 93; Gaps 10;

QY	400	CYTCGCTCTGAGTGGTATGGAATATCTCTACGTGGGGCTGAGAGCCATCTCGG	459
DB	53	CCCTTCTGTGAGCAGGATGGAAGACGCTGTGTGTGGGGCCCGAGAGGCCCTCTTG	112
QY	460	CCTTGATATCAGGATCCAGGGGTCCC---CAGGCTAAAGAACATGATACCGTGGCCAG	516
DB	113	CACCTTAACAGCAACCTCAGCTTCTTCCAGGGGGGAGTACCAAGAGCTACTGTGGAGTG	172
QY	517	CCAGTCACAGAAAAAGAGTGAATGCTTTTAAAGAGAGCAATGAGACACAGTGT	576
DB	173	CAGATCTCAGAGGAAGCAGCAGTGCAGCTTCAAGGGCAAGGACCCAAAGCGTACTGTC	232
QY	577	TCAACTTCATCCGTGTCTGTTTCTTCAATGTCAACATCTTACACCTCGGCACCT	636
DB	233	AAACTACATCAGATCTCTCCACTCAACAGAGCCACTGCTCACTGTGGCAGG	292
QY	637	TGCGCTTCAGCCCTGCTGTACTCTTCATGTAACTCAAGATTCCTACCTGTGCCATCT	696
DB	293	CGCCCTTCAGCCCTGCTGTGTCTTACATTCATCAGCAGCTTTACTTTAGCCCAAGATG	352

QY 697 CGAGAGCAAGGTCAAT-----GAGGGGAAAGGCGAAGGCCCTTTGACCCCGCTCACA 750
 Db 353 AGCCCGGTAAATGTCAATCTCTGGAGGATGGCAAGGGTCAATGTCCCTTTGACCCCAACTTCA 412
 QY 751 AGCATACGGCTGTCTTGGTGGATGGATCTCTATCTGTGTACTATGAACAACACTTCTCTGG 810
 Db 413 AGTCCACGGCTGTGGTGGTGTGATGTGAGTGTACACTGGAACAGTCACTAGTCTCCAGG 472
 QY 811 GCAGTGAAGCCCATCTCTGATGCGGACACTCTGGGATCCAGAGCTCTCTCAAGACCGCAACT 870
 Db 473 GAAACGACCCAGCCATTTCCCGAGGACAGATTCGCGGCC---CACCAAGACTGAGAGCT 529
 QY 871 TCCCTCCGTGGCTGATCATGATGAGCCCTCTTGTGTGGACCCATCCCTTCGACCCAGGTCG 930
 Db 530 CCTCAACTGGCTACAAGACCCCTGCTTGTGGCTCTGGCTACGTCCTCCCGAGAGCTCGG 589
 QY 931 -----TCTACTCTCTTCTTCCAGAGAGACAGACCGAGT 963
 Db 590 GCAGCCCCATAGGTGATGATGATAAGATCTACTTCTTCTTCCAGCGAGACGGGCCAGGAGT 649
 QY 964 TTGACTTCTTTGAGAGGCTCCACACATCGGGTGGCTAGAGTCTGCAAGATGACGTGG 1023
 Db 650 TTGAGTCTTTGAGAACACCATCGTCTCGGAGTTGCCGAGTCTGTAAAGGCGGATGAG 709
 QY 1024 GCGGCGAAAGCTGCTGCGAAGAGTGAACCACTTCTCTGAGGCCAGCTGCTCTGCA 1083
 Db 710 GTGGAGAGCGGGTGTTCGACCAACGCTGGACCTCTTCTCAAGGCTCAGCTCTCTGTGCT 769
 QY 1084 CCAGCGGGGCA--GCTGCCCTTCAAGTCACTCGCCAGCGGTCCTGTCTCCCGCGC 1140
 Db 770 CCGGGCTGATGATGGGTCTTCCCTTTAACTGTCTCAAGATGCTTCACTCCCTGAACCCCA 829
 QY 1141 ATTCTCCACAGCTCCCCACATCTA-----CCAGTCTTCACTCCAGTGGCGAGTTG 1194
 Db 830 ACCCTCAGGATTTGGCGCAAGACCTTTCTATCGGGTCTTTACTCCCTCCAGTGGCACAGAG 889
 QY 1195 GCGGACAGAGCTCTCGGTTGTGCTTCTCTCTCTGACATGTAAGCTGTCTTTA 1254
 Db 890 GGACCAAGAGGCTCTGCGTCTTCCCTTCACTGATGATGTGCAAGGCGCTTTG 949
 QY 1255 AGGGGAATCAAGAGTGTGAACAAGAACTTTCAGCTGGACTTATATAGGGGCGCTG 1314
 Db 950 ACGCCCTGTACAGAAAGTAAACAGAGAGACACAGCAGTGGTATACGAGACCCACAGG 1009
 QY 1315 AGACCAACCCCGGCCAGGAGTTG-----CT 1341
 Db 1010 TGCCCAACACCGCGCGCGGAGCGTGCATTACCAACAGTCCCGGGAACGGAAGATCAACT 1069
 QY 1342 CAGTGGGCCCTCTCTCTGATAAGGCCCTTGACCTTTCATGAAGGACCATTTCTCTGATGATG 1401
 Db 1070 CGTCCCTGCAGCTCCAGACCGAGTGTGAATCTTCTCAAGGATCACTTCTGATGATG 1129
 QY 1402 AGCAAGTGGTGGGACCGCCCTGTGTGTGAATCTGCGCTGGAGTATACAGGCTTGCAG 1461
 Db 1130 GGCAGGTCGCGAGTCTGCTGTCTGTCTGAGCCAGAGCCGCTACCAAGCTGTGGCTG 1189
 QY 1462 TGGAGACAGCCAGCGCTCTGATGGGACAGCCATCTTGTCTGATCTCTGGGAACCAACCA 1521
 Db 1190 TGCACCGTGTCTGGCTGACAG---CACTATGATGTCTTCTTCTGGCAGTGGTG 1246
 QY 1522 CAGGCTCGCTCCACAAAGCTGTGTAAAGTGGGAGCAGAGTGTCTATCTGGTGGAGAGA 1581
 Db 1247 ATGGCGGCTGCACAAAGCAGTG---ACCTGTAGCTCCAGATCCACATCATTTGAGAGC 1303
 QY 1582 TTCAGCTGTCTCCCTGACCCCTCAACTGTTCGCAACCTGCAAGTGGCCCGCCACCCAGGGTG 1641
 Db 1304 TGCAGATCTTCTCAAGGACAGCTGTGAGAACCTTGTCTTGGACAGCATATGGGGAC 1363
 QY 1642 CAGTGTCTTGTAGGCTCTCAAGAGGTGTCTGGAGGGTGGCCCGGAGCCCACTGTAGTGTCT 1701
 Db 1364 TGTGTATGCTCTCTCCCATTTCCGGGGTGGTGGTGAAGTGGCCGCTGACCAACTGCGAGCTGT 1423

QY 1702 ATGAGAGCTGTGTGGACTGTGTCTTGGCCGGGAGCCCCACACTGTGTGCTGGGACCCCTGAGT 1761
 Db 1424 ACCCACTGTGTGAGACTGCCCTCTGCTCGAGACCCCTACTTGGCTGGACTGGCTCTG 1483
 QY 1762 CCGAACCCTGTTCCTCTGTCTGCCCCCAACCTGAACTCTCTGGAAGCAGGACATGGAGC 1821
 Db 1484 CCTGCGAGGCTCGCTAGCTCTTACAGCCTGTATGCGCTTCCAGGGCCATGGACCCAGGACA 1543
 QY 1822 GGGGGAACCCAGAGTGGGATGTGCCAGTGGGCCCATGAGCAGGAGCCTTTGGCCCTCAGA 1881
 Db 1544 TTGAGGCTGCAGTGTCAAGGAATCTGCAAGAAATTTCTCATACAAGGCCCGGTTCTTG 1603
 QY 1882 GCGCCCGCAAAATCATTAAGAAAGTCTGTGCTGTCTCTTCACTCTCTGAGAGCTCCCT 1941
 Db 1604 TGCAGGTAAGCCATGTAAACAAGTCCAGATCAACCAACAACAGTGAACACCCCTGGCT 1663
 QY 1942 GCGCCACCTGTGAGCCTTGGCTCTTATTTATGAGTCTATGCGCCAGCAGCAGTCCCA 2001
 Db 1664 GCGCACTCTCTCAACCTTGGCCACTCGGCTCTGGGTGCAATGAGGCCCACTCAATG 1723
 QY 2002 AAGCCTCTTCACTGTCTA-----CAATGGCTCCCTCTTGTCTGATGATGCGAGTGGAG 2055
 Db 1724 CCTCTGCTCTCTGCGGCTGTATTACCCACCGGGGACCTGCTGTGGTGGGCGAGCAGAG 1783
 QY 2056 TTGGGGTCTCTACAGTGTGGCAACTGAGAATGGCTTTTCATACCTCTGTGATCTCT 2115
 Db 1784 GTTTGGGGTGTTCAGTGTGGTGTGATGAAGAGGATTCAGCAGCTTGTGGCCAGCT 1843
 QY 2116 ACTG 2119
 Db 1844 ACTG 1847

RESULT 2
 US-08-556-422A-1
 ; Sequence 1, Application US/08556422A
 ; Patent No. 6576754
 ; GENERAL INFORMATION:
 ; APPLICANT: FREEMAN, Gordon J.
 ; APPLICANT: SCHULZE, Joachim L.
 ; APPLICANT: BOUSSIOTIS, Vassiliki
 ; APPLICANT: NADLER, Lee M.
 ; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING CD100 MOLECULES
 ; FILE REFERENCE: DFN-005CPA2
 ; CURRENT APPLICATION NUMBER: US/08/556,422A
 ; CURRENT FILING DATE: 1995-11-09
 ; NUMBER OF SEQ ID NOS: 7
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 1
 ; LENGTH: 4157
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (88)...(2673)
 US-08-556-422A-1

Query Match 4.4%; Score 153.4; DB 4; Length 4157;
 Best Local Similarity 50.0%; Pred. No. 5.2e-32;
 Matches 743; Conservative 0; Mismatches 636; Indels 108; Gaps 10;

QY 369 TTCACCAAGAGGCGCTCCAGGATTTTGACACTCTGCTCTGAGTGGTGGTGAATAACT 428
 Db 211 TTTCATGAGCCAGACATCTCAACTACTCAGCTTGTCTGAGCGGAGCAAGGACACC 270
 QY 429 CTCTACGTGGGGCTTCGAGAAGCCATTCTGCGCTTGGATATCCAGGATCCAGGGGTCCCC 488
 Db 271 TTGTACATAGGTGCGCGGAGGC-----GGTCTTGGCTGTGAGCGCACTCAACATCTCC 324
 QY 489 AGGCTAAGAACATGATATACCGTGGCCAGTGCAGAAAAAGAGTGAATGTGCTCTT 548
 Db 325 GAGAAAGCAGTATGAGTGTATTGGAGGTCTCAGAAGACAAAAAGCAAAATGTGCAGAA 384

QY 549 AAGAAGAGAGCAATGAGACACAGTGTTCAACTTCATCCGTGCTCCTGTTCTTACAAAT 608
Db 385 AAGGGGAATCAAAACAGACAGAGTGCCTCACTACATCGGGTGTGTCAGCCACTCAGC 444
QY 609 GTCAACCAATCTTACACCTGCGGCACTTGGCCCTTCAGCCCTGCTGTGACCTTCATTGNA 668
Db 445 GCCACTTCCCTTTACGTGTGTGGGCAACAGCAATCCAGCCGCTGTGACCACTGAAAC 504
QY 669 CTTCAAGATTCTTACCTGTTGCCATCTCGAGGACAAAGGTCAATGAGAGGAAAGGCCAA 728
Db 505 TTAACATCTTTAAGTTTCTGGGGAATAATGAAT-----GGCAAGGAAGA 552
QY 729 AGCCCTTTGACCCGCTCAAGACATACGGTGTCTTGTGTGATGGATGCTTATTCT 788
Db 553 TGTCCCTTTGACCCGACACACAGCTACACATCGGTGATGTTGATGGAGAACTTTATTCTG 612
QY 789 GGTACTATGACAACTTCTTGGGAGTGGCCATCTGATGCGACACTGGGATCCCAAG 848
Db 613 GGGACGTGCTATTAATTTTTTGGGAAGTGAACCATCATCTCCGAAATCTTCCACAGT 672
QY 849 CCTGTCTCAAGACCGCAAACTTCTCCGCTGGCTGATCATGACGCTCTCTTTTGGCA 908
Db 673 CCTCTGAGGACAGAAATGCAATCCCTTGGCTGAACGAGCTAGTTTCTGTGTTGCTGAC 732
QY 909 GCCATCCCTTGCACCCAGTCT-----GTCTACTTCTTCTTC 944
Db 733 GTGATCGGAAAGCCAGACAGCCCGAGCGGAGGATGACAGGCTCTACTTCTTCTTC 792
QY 945 GAGGAGACAGCCAGCGAGTTTGTACTTCTTTGAGAGGCTCCACATGCGGGTGGCTAGA 1004
Db 793 ACGAGGTGTCTGTGGAGTATGAGTTTGTTCAGGGTGTGATCCACCGATAGCAAGA 852
QY 1005 GTCTGCAAGATGAGTGGGGGGAAGCTGCTGAGAGAGTGGACCACTTCTCTG 1064
Db 853 GTGTGCAAGGGGACCGAGGGGGCTGAGGACCTTGAGAGAAATGGACCTCTTCTCTG 912
QY 1065 AAGCCCAAGCTGTCTGCAACCCAGCCG---GGCAGCTGCCCTTCAACGTATCCGCCAC 1121
Db 913 AAGCCCGACTCATCTGCTCCCGCCAGACAGCGCTTGGTCTTCAATGTGCTGCGGAT 972
QY 1122 GCGTCTGTCTCCCGCGGATCTCCACAGCTCCCACTCCCACTACGAGCTTCACTCC 1181
Db 973 GTCTTCTGTCTCAGTCTCCCGGGCTGAAGGTGCTGTGTTATGCACTCTTCAACCCCA 1032
QY 1182 CAGTGGCAGGTGCGGGACCAAGAGCTCTGCGGTTTGTGCTTCTCTCTTGGACAT 1241
Db 1033 CAGCTGAACAGCTGGGCTGTGCGAGTGTGCGCTTCAACCTGTC---CACAGCCGAG 1089
QY 1242 GAACGTGTCTTTAAGGGGAATAAAGAGTTGAACAAAG-----AAACTTCAGC 1292
Db 1090 GAGGTCTTCTCCACGGGAAGTACATGACAGACACCAAGTGGAGCACTCCACCAAG 1149
QY 1293 TGGACTACTTATAGGGCCCTGAGACCAACCCCGCCAGGCACTGTGCTCAGTGGG--- 1349
Db 1150 TGGTGGCTATATGGCCCGGTACCCAAAGCGGGCTGTGAGGCTGATCGACAGGAG 1209
QY 1350 -----CCCTCTCTGTATAGGCGCTGACCTTCAATG 1379
Db 1210 GCACGGGCGCCAACTACACAGCTCTCTTGAATTTGCCAGACAAGACGCTGAGTTGTT 1269
QY 1380 AAGGACCAATTTCTGATGATGA-----GCAAGTGTGGGAGCCCTCTGCTG 1430
Db 1270 AAGAACCACTTTTATGATGATGATCGGTAAACCCCAATAGACAACAGCCCGAGTTAATC 1329
QY 1431 AAATCTGGCGTGGATATACAGGCTTGCAGTGGAGACAGCCAGGGCTTGTATGGGAC 1490
Db 1330 AAGAAAGATGTAACTACACCCAGATCGTGTGGACCGAGCCAGCCCTGGATGGAGT 1389
QY 1491 ACCCATCTTGTATGATCTGGAGACCAACAGGCTGCTCCCAAGAGGTGTGTAAGT 1550
Db 1390 GTCTATGATGTATGTTTGTGACGACAGACCGGGAGCTCTGCAAAAGCAATC---AGC 1416

QY 1551 GGGACAGCAGTGTCTATCTGTGGAGATTACAGTTCAGCTGTTCCCTGACCCCTGAACCTGTT 1610
Db 1447 CTCGAGCACCGTGTTCATCATATCGAGGACCCAGCTCTTCCAGGACTTTCAGCAATC 1506
QY 1611 CGCAACCTGACAGCTGGCCGCCACCCAGGGTGCAGTGTGTTGT-----AGGCTTCTCAGGA 1664
Db 1507 CAGACCTGCTGTGCTTCTCAAGAGGGCAACAGAGTTTGTCTATGCTGGCTCTTAACCTG 1566
QY 1665 GGTGTGTGAGGGTGGCCCGAGCCAACTGTAGTGTCTATGAGAGCTGTGTGAGCTGTGTC 1724
Db 1567 GCGTGTGTTCAGGGCCCGCTGCGCTTCTGTGGGAAGCACGCACTCGAGGATGTGTG 1626
QY 1725 CTTGCCCGGGACCCCACTGTGCTGGGACCCCTGAGTCCCGAACCTG 1771
Db 1627 CTGGCGGGAGCCCTACTGCGCTGGAGCCCGCCACAGGACCTG 1673

RESULT 3
US-09-077-940A-3
; Sequence 3, Application US/09077940A
; Patent No. 6576441
; GENERAL INFORMATION:
; APPLICANT: KIMURA, Toru et al.
; TITLE OF INVENTION: NOVEL SEMAPHORIN Z AND GENE ENCODING THE SAME
; FILE REFERENCE: 0020-4426P
; CURRENT APPLICATION NUMBER: US/09/077,940A
; CURRENT FILING DATE: 1998-06-05
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 3524
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: 5'UTR
; LOCATION: (1)..(38)
; OTHER INFORMATION:
; NAME/KEY: 3'UTR
; LOCATION: (2706)..(3524)
; OTHER INFORMATION:
; NAME/KEY: CDS
; LOCATION: (39)..(2702)
; OTHER INFORMATION:
US-09-077-940A-3

Query Match 3.6%; Score 126; DB 4; Length 3524;
Best Local Similarity 55.3%; Pred. No. 1.9e-24;
Matches 315; Conservative 0; Mismatches 240; Indels 15; Gaps 3;

QY 549 AAGAAGAGCAATGAGACACAGTGTTCAACTTCATCCGTGCTCCTGTTCTTACAAAT 608
Db 390 ATGAAGGGCAACAGAGGGCGAGTGTGAAACTTCGTAAGGTGCTGCTCCTCGGAC 449
QY 609 GTCAACCAATCTTACACCTGCGGCACTTGGCCCTTCAGCCCTGCTGTGACCTTCATTGNA 668
Db 450 GAGTCCACGCTCTTGTGTGCGGTTCCAAAGCGCTTCAACCCGCTGTGCGCCAACTACAG 509
QY 669 CTTCAAGATTCTTACCTGTTGCCATCTCGGAGGACAAAGTTCATGAGAGGAAAGGCCAA 728
Db 510 ATAGA-----CACCTCGAGCCCGCTCGAGACA-----CATCAGCGTATGGCCCG 557
QY 729 AGCCCTTTGACCCCGCTCAAGACATACGGTGTCTTGGTGGATGGGATGCTCTATTCT 788
Db 558 TGCCCGTACGACCCCAAGCACGCAATGTTGCCCTTCTCTGACGGGATGCTCTTCA 617
QY 789 GGTACTATGAACAACTTCTCGGCACTGAGCCCATCTGATGCGCACACTGGGATCCCAAG 848
Db 618 GCTACTGTTACCGACTTCTTAGCATTGATGTGTCATCTACCGAGCTTCGGGACAG 677
QY 849 CTTGTCTCAAGACCGACAACTTCTCCGCTGGCTGTCATCATGACGCCCTCTTTTGGCA 908
Db 678 CCACCCCTGGCAGCCCTGAAACATGACTCCAAGTGTTCAAAGAGCTTACTTTGTCCAT 737

QY 909 GCATCCCTTCGACCCAGGTCGTCTACTTCTTCGAGGACAGACAGCCAGCGAGTTGAC 968
Db 738 GCGGTGAGTGGGGCAGCCATGCTACTTCTTCTCCGGAGATTGCGATGAGTTTAAAC 797
QY 969 TTCTTTGAGAGGTCACACATCGCGGTGGCTAGAGTCTGCAAGAAATGACGTGGCGGC 1028
Db 798 TACTGGAGAGGTGGTGGTGTCCCGGTGGCCGAGTGTGCAAGAACGACGTGGGAGC 857
QY 1029 GAAAGC---TGTCGAGAGAGTGGACACCTTCTGAAAGCCAGCTGCTTGCACC 1085
Db 858 TCCCCCGCGTGTGGAGAGCAGTGCAGCTCTCTCTGAAAGCGCGGTCAACTGCTCT 917
QY 1086 CAGCGGGGAGCTGCCCTTCAACGTCATC 1115
Db 918 GTACCGGAGACTCCCATTTCTACTTCAAC 947

RESULT 4

US-09-077-940A-1
; Sequence 1, Application US/09077940A
; Patent No. 6576441
; GENERAL INFORMATION:
; APPLICANT: Kimura, Toru et al.
; TITLE OF INVENTION: NOVEL SEMAPHORIN Z AND GENE ENCODING THE SAME
; FILE REFERENCE: 0020-4426P
; CURRENT APPLICATION NUMBER: US/09/077,940A
; CURRENT FILING DATE: 1998-06-05
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 3692
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; FEATURE:
; NAME/KEY: 5'UTR
; LOCATION: (1)..(18)
; NAME/KEY: CDS
; LOCATION: (19)..(2682)
; OTHER INFORMATION:
; NAME/KEY: 3'UTR
; LOCATION: (2683)..(3653)
; OTHER INFORMATION:
; NAME/KEY: PolyA site
; LOCATION: (3654)..(3692)
; OTHER INFORMATION:
US-09-077-940A-1

Query Match 3.6%; Score 125.4; DB 4; Length 3692;
Best Local Similarity 58.5%; Pred. No. 2.8e-24;
Matches 238; Conservative 0; Mismatches 166; Indels 3; Gaps 1;
QY 710 CATGAGGAGAAAGCCCAAGCCCTTTGACCCCGCTCAAGATACGCTGCTTGGT 769
Db 522 CATCAGTGGTATGGCCGCTCCCTACGACCCCAAGCATGCCAATGTCGCCCTCTTC 591
QY 770 GGATGGGATGCTATTCTGTGCTATGAAACAATCTCTGGGAGTGGAGCCATCTCGAT 829
Db 582 AGATGGGATGCTTCTACAGCCACAGTAACTGACTTCTTAGCCATGACGCTGTATCTA 641
QY 830 GCGCACACTGGGATCCCAAGCTGCTTCAAGACGACAACTTCTCCGCTGGCTGCAATCA 889
Db 642 CCGTAGCCTTGGGACCCGCGCCACACTGCGCACAGTAAAGCATGACTCCAAAGTGGTTAA 701
QY 890 TGAGCCTCTTGGGAGCAGCCATCCCTTTCAGCCAGTGTCTTCTTCTTCGAGGA 949
Db 702 AGAGCCATCTTGTGATGCGGTGGAGTGGGAGCCAGCTCTACTTCTTCTTCGCGGA 761
QY 950 GACAGCCAGGATTTGATCTTTTGGAGGCTCCACATCGCGGTGGCTAGAGTCTG 1009
Db 762 GATCGCCATGGAGTTTAACTATCTGAAAAGGTGTGTGTGTCCTGTCGCGCCGTGTATG 821
QY 1010 CAGAAATGACGTGGGCGG---CGAAAAGCTGTCGAGAGAGTGGAGCCACCTTCTCTGAA 1066

Db 822 CAAGAAATGATGTGGCGGCTCCCAACGGGTGCTGGAGAACGAGTGGACTTCTTCTGAA 881
QY 1067 GCGCCAGCTGCTGCAACCCAGCGGGGAGCTGCCCTTCAACGTCA 1113
Db 882 GCGCCGCTCAACTGCTCCGCTGGGACTCACACTTCTACTTCA 928

RESULT 5

US-09-976-594-1002
; Sequence 1002, Application US/09976594
; Patent No. 6673549
; GENERAL INFORMATION:
; APPLICANT: Buchbinder, Michael
; TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS
; FILE REFERENCE: PA-0041 US
; CURRENT APPLICATION NUMBER: US/09/976,594
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: 60/240,409
; PRIOR FILING DATE: 2000-10-12
; NUMBER OF SEQ ID NOS: 1143
; SOFTWARE: PERL Program
; SEQ ID NO 1002
; LENGTH: 2278
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6673549 411373.7
US-09-976-594-1002

Query Match 2.9%; Score 102; DB 4; Length 2278;
Best Local Similarity 50.0%; Pred. No. 6.4e-18;
Matches 339; Conservative 0; Mismatches 330; Indels 9; Gaps 3;
QY 717 GAAAAGGCCAAAGCCCTTTGACCCCGCTCACAAGCATACGGCTGCTTGGTGGATGGG 776
Db 761 GGAATGCCAGATGCCCATATGATGCCAAACATGCCAAGCTTGCTGTTTGCAGATGA 820
QY 777 ATGCTTATTTCTGGTACTATGAACAATCTCTGGGAGTGGAGCCATCTTATGCGGACA 836
Db 821 AAACCTATATCTCAGCCACAGTACGATCTCTCTCCATTTGACGAGTCAITTTACCGAGT 880
QY 837 CTGGATCCAGCTGCTCTCAAGACGACAACTTCTCCGCTGGCTGCATCATGAGCC 896
Db 881 CTGGAGAAAGCCCTTACCTCGGAGCCGTCAAGCAGATTCAAATGTTGAAAGAACCA 940
QY 897 TCCTTTGTGGCAGCATCCCTTTCGACCCAGTGTCTACTTCTTCTTCTTCGAGGACAGCC 956
Db 941 TACTTTGTTCAAGCGTGGATTACGGAGATTATATCTACTTCTTCTTTCAGGAAATACCA 1000
QY 957 AGCGAGTTTGAATCTTTTGGAGGCTCCACACATCGCGGTGGCTAGAGTCTGCAAGAAAT 1016
Db 1001 GTGGAGTATTAACACATGGGAAAGTAGTCTTCCAGAGTGGCTCAGGTTTGTAAAGAT 1060
QY 1017 GACGTGGGCGG---CGAAAAGCTGTCGAGAAAGTGGACCACTTCTCTGAAGCCCGAG 1073
Db 1061 GATATGGAGGATCTCAAAAGAGTCTCTGAGAAACAGTGGAGCTGCTTCTCTGAAGCGCGC 1120
QY 1074 CTGCTCTGCACCCAGCGGCGAGCTGCCCTTCAACGTCATCCGCGAGCGTCTGCTC 1133
Db 1121 TTGAATCTGCTAGTTCTTGGAGACTCTCTCATTTTATTTTCAACATTTCTCAGGAGTACA 1180
QY 1134 CCGCGCGATTTCTCCCAAGCTCCCAATCTACGAGTCTTCACTCCAGTGGCAGGTT 1193
Db 1181 GATGTGATTCTGATCAACGGGCGTGAATGT---TGTCCTGGCAACGTTTTTCTACACCTTAT 1237
QY 1194 GCGGAGCAGGAGCTGCGGTTTGTGCTTCTCTCTTGGACATTTGAAGCTGCTCTT 1253
Db 1238 AACAGCATCCCTGGGTGTCAGTCTGTGCTTATGACATGCTTGTGATTTGCCAGTGT 1297
QY 1254 AAGGGGAAATACAAAGAGTGTGAACAAAGAACTTCAACGCTGGAGTAC---TTATAGGGGC 1310

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Db      1298 ACTGGGAGATTCAAGAAACAGAGTCTCTGATTCCACCTGGACACCAAGTTCTCTGATGAA 1357
QY      1311 CCTGAGACCAACCCCGCCAGGACGATTGCTCAGTGGGCCCTCTCTGTGATAAGGCCCTG 1370
Db      1358 CGAGTTCTTAAGCCAGCCAGGCTGCTGTGCTCATCTCTCTTAGAAGATATGCA 1417
QY      1371 ACCTTCATGAAGACCAT 1388
Db      1418 ACCTCCATGAGTTCCT 1435

```

RESULT 6

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US-09-833-381-202
; Sequence 202, Application US/09833381
; Patent No. 6672186
; GENERAL INFORMATION:
; APPLICANT: Robison, Keith E.
; TITLE OF INVENTION: No. 6672186el Nucleic Acid and Protein Homologs
; FILE REFERENCE: 5800-119
; CURRENT APPLICATION NUMBER: US/09/833,381
; CURRENT FILING DATE: 2001-04-11
; PRIOR APPLICATION NUMBER: 09/516,448
; PRIOR FILING DATE: 2000-02-29
; NUMBER OF SEQ ID NOS: 2050
; SOFTWARE: PastSeq for Windows Version 3.0
; SEQ ID NO 202
; LENGTH: 121
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-833-381-202

```

```

Query Match      2.8%; Score 98.6; DB 4; Length 121;
Best Local Similarity 88.4%; Pred. No. 1.1e-17;
Matches 107; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY      893 CGCTCTTGTGGCAGCATCCCTCGACCCAGTCTCTACTTCTTCTTCGAGGAGAC 952
Db      1 CGCTCTTGTGGAGAGATCCCTCTACCCAGCGGCTACTTCTTCTTCAGGAGAC 60

QY      953 AGCCAGCGAGTTGACTTCTTTGAGAGGCTCCACACATCGGGGTGGCTAGAGTCTCAA 1012
Db      61 AGCCAGCGAGTTAGACTCTTTTGGAGGCTCCACACATAGTTGGTAGAGTCTGCA 120

QY      1013 G 1013
Db      121 G 121

```

RESULT 7

```

US-09-254-594-5
; Sequence 5, Application US/09254594
; Patent No. 6566094
; GENERAL INFORMATION:
; APPLICANT: KIMURA, Toru
; APPLICANT: KIKUCHI, Kaoru
; TITLE OF INVENTION: NOVEL SEMAPHORIN GENE: SEMAPHORIN Y
; FILE REFERENCE: 0020-4527P
; CURRENT APPLICATION NUMBER: US/09/254,594
; CURRENT FILING DATE: 1999-05-11
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 5
; LENGTH: 2790
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(1)
; OTHER INFORMATION: Tissue Type: Child Brain
; NAME/KEY: CDS
; LOCATION: (1)..(2790)
; OTHER INFORMATION: Identification Method: E

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; NAME/KEY: misc feature
; LOCATION: (1)..(1)
; OTHER INFORMATION: Identification Method: P for resulting peptide
US-09-254-594-5

Query Match      2.8%; Score 98.6; DB 4; Length 2790;
Best Local Similarity 50.1%; Pred. No. 6.3e-17;
Matches 369; Conservative 0; Mismatches 344; Indels 24; Gaps 4;

QY      571 AGTGTTCACATTCATCCGTGCTCTGTTGATCACTTCTTCAATGTCACCCATCTCTACACCTGGC 630
Db      359 AGTGTACAACTATATTCGTGTTGTTGCTCCCTGGGACTCCAGACAGCTCTCTGCTGTG 418
QY      631 GCACCTTCGCTTCAGCCCTCTGTTGATCACTTCTTCAATGTCACCTTCAAGATTCCTACCTGTTC 690
Db      419 GAACGAATCTATTGAGCCCTCTGTTGCGCCAGCTATGGAT-----AATTCGC 466
QY      691 CCATCTCGGAGSACAAGTCTCATGAGGGAAGGCAAGCCCTTTGACCCCGCTCACA 750
Db      467 TGCAGCAGGAGGTGAGGAAGTGAAGTGGGCGGCTCGATGCCCTTTGATGCCACCCAGT 526
QY      751 AGCATACGGCTGTCTTGGTGGATGGGATGCTCTATTCTGTGTAATGTAACAACATTCCTCG 810
Db      527 CCAACGTGGCCATCTTTCAGAGGGGCGCTGTACTCAGCCACAGCTGCGGATTTCCAGG 586
QY      811 GCAGTGGCCCATCTCTGATGGGACACCTGGGATCCGACCTGTCTCTCAAGACCGACAAT 870
Db      587 CCAAGTGTGCTGTAGTTTACAGAAAGCTTGGGGCCCGCCCACTCCGCTCCGCCAAGT 646
QY      871 TCCTCCGTGGCTGCATCATGACGCTCTCTTTGTTGGCAGCCATCCCTTCGACCCAGGTGC 930
Db      647 ATGACTCCAAAGTGGCTCCGAGAGCCACACTTTGTCAGGCTTGGAGCATGGAGCCATG 706
QY      931 TCTACTTCTTCTCGAGGAGACAGCCAGCGAGTTTGACTTCTTTGAGAGGCTCCACACAT 990
Db      707 TCTACTTCTTCTTCGCGAGGTCTCTGTGGAGGATGCTCGGCTGGGGAAAGGTGCACTTCT 766
QY      991 CCGGGGTGGCTAGAGTCTGCAAGAAATGACGTGGGCGGCGGCAAAAGCTG---CTGCAGAGA 1047
Db      767 CCGCGTAGCCGAGTATGTAACGTGACATGGGCGGCTCGCTCGGCGCTTGGACCGCC 826
QY      1048 AGTGACACCATCTCTGAGGCCAGCTGCTGACCCAGCGGCGGCGGCGGCGGCGGCGGCTTCA 1107
Db      827 ACTGACATCTCTCTGAGGCTTCGGGTCAACTCTCTGTCCCTGGGAGTCTACTTTCT 886
QY      1108 A---CGTCATCCGCCAGCGGTCTCTGCTCCCGCGGATTTCTCCACAGCTCCCCACATCT 1164
Db      887 ATTTTGATGTTTACAGSCCTTGACTGGGCTGTGAACCTGTCATGGCGGCTCTGCTCTCT 946
QY      1165 AGCAGTCTTCACCTCCAGTGGGAGGTTGGCGGAGCAGGAGCTCTGCGGTTGTGCT 1224
Db      947 TTGGGGTCTTCACCAACCAGACCAA-----TAGCATCCCTGGCTCTGCGCTGTGCGCT 1000
QY      1225 TCTCTCTCTGGACATTCAGCTGTCTTTAAGGGGAATACAAAGAGTTGAACAAGAAA 1284
Db      1001 TCTACCTGGATGAGATTGAGGTTGGGTTTGAGGGCAAGTTTCAAGGAGCAGAGGATCTGG 1060
QY      1285 CTTGACGCTGGACTACT 1301
Db      1061 ATGGGGCTGGACTCCT 1077

RESULT 8
US-09-254-594-4
; Sequence 4, Application US/09254594
; Patent No. 6566094
; GENERAL INFORMATION:
; APPLICANT: KIMURA, Toru
; APPLICANT: KIKUCHI, Kaoru
; TITLE OF INVENTION: NOVEL SEMAPHORIN GENE: SEMAPHORIN Y
; FILE REFERENCE: 0020-4527P
; CURRENT APPLICATION NUMBER: US/09/254,594
; CURRENT FILING DATE: 1999-05-11

```

NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 3432
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1..7)
; OTHER INFORMATION: Tissue Type: Child Brain
; NAME/KEY: 5'UTR
; LOCATION: (1..187)
; OTHER INFORMATION: Identification Method: E
; NAME/KEY: misc feature
; LOCATION: (188)..(2977)
; OTHER INFORMATION: CDS; Identification Method: E
; NAME/KEY: 3'UTR
; LOCATION: (2978)..(3407)
; OTHER INFORMATION: Identification Method: E
; NAME/KEY: PolyA signal
; LOCATION: (3408)..(3432)
; OTHER INFORMATION: Identification Method: E
US-09-254-594-4

Query Match 2.8%; Score 98.6; DB 4; Length 3432;
Best Local Similarity 50.1%; Pred. No. 7.1e-17;
Matches 369; Conservative 0; Mismatches 344; Indels 24; Gaps 4;

QY 571 AGTGTTCACATTCATCGGTGCTGTTCTTACATGTCACCCATCTCTACACCTGCG 630
DB 546 AGTGCTACATATATCGTGTCTTCTTCCCTGGGACTCCAGAGCGCTCTTGCCTGTG 605
QY 631 GCACCTTCGCTTCAGCCCTGCTGTACTCTTCACTTCAAGATTCAGATTCCTACCTGTGC 690
DB 606 GAAGCACTCATTCAGCCCTGTGTGCGCAGCTATGGAT-----AATTCGC 653
QY 691 CCATCTCGAGGACAAGTCTATGAGGGAAGGCAAGCCCAAGCCCTTTGACCCGCTCACA 750
DB 654 TGCAGCAGGAGGTGAGGAACATGATGCGGAGGCTCGATGCCCTTTGATGCCACCCAGT 713
QY 751 AGCATAGCGTGTCTGTGTGATGGGATGCTCTATTCTGTGACTATGAACAATCTCTGG 810
DB 714 CCAAGTGGCCATTTTGCAGAGGCGACCTGTACTCAGCCACAGCTCGGATTTCCAGG 773
QY 811 GCAGTGAAGCCCATCTGATGCGCACAATGGGATCCAGCCTGTCTCAAGACCGACAAT 870
DB 774 CCAGTGATGCTGTAGTTTACAGAAGCCTTGGGCCCCAGCCCCCACTCCGCTCCGCCAAGT 833
QY 871 TCCTCCGCTGGCTGATCATGACGCTCTTTTGTGGCAGCCATCCCTTCGACCCAGGTG 930
DB 834 ATGACTCCAAAGTGGCTCCGAGAGCCACACTTTTGCAGGCTTTGGAGCATGGAGACCATG 893
QY 931 TCTACTTCTTCTTGAGGAGACAGCCAGAGTTTGACTTTTGTGAGAGGCTCCACAT 990
DB 894 TCTACTTCTTCTTCGCGAGGTCTCTGTGGAGGATGCTCGGCTGGGGAAGGTGCAATTCT 953
QY 991 CGCGGTGGCTAGATCTGCAAGATGACGTGGGCGGGAAGACTG---CTGCAGAGA 1047
DB 954 CCCGGTAGCCGAGTATGTAACGTGATGAGCGGCTCGCCCTCGGCGCTTGACCGCC 1013
QY 1048 AGTGACACACCTTCTGAAGGCCAGCTGCTCTGACCCAGCCGCGGCGAGCTGCCCTTCA 1107
DB 1014 ACTGACATCTTCTTGAAGCTTCGGCTCAACTGCTCTGCTCTGCTGGGACTCTACTTCT 1073
QY 1108 A---CGTCATCGGCAAGCGGTCTGTCTCCCGCGGATTTCTCCACAGCTCCCACTCT 1164
DB 1074 ATTTTGTATGTTTACAGGCCCTTGAATGGGCGTGTGAACCTGCATGGCGGCTCTGCTCT 1133
QY 1165 AGCGAGTCTTCACTTCCAGTGGCAGGTTGGCGGACCCAGAGCTCTGCGGTTTGTGCT 1224
DB 1134 TTGGGGTCTTACACACCCAGACCA-----TAGCATCCCTGGCTCTGCGCTCTGCGCT 1187
QY 1225 TCTCTCTCTTGACATTTGAACGTGTCTTTAAGGGGAATATCAAGAGTTGAACAAAGAA 1284

DB 1188 TCTACCTGATGAGATTGAGCTGGTTTGAAGGCAAGTTCAAGGACGAGGAGTCTGG 1247
QY 1285 CTTTACCGCTGGACTACT 1301
DB 1248 ATGGGGCTGGACTCCT 1264

RESULT 9
US-09-254-594-2
; Sequence 2, Application US/09254594
; Patent No. 6566094
; GENERAL INFORMATION:
; APPLICANT: KIMURA, Toru
; APPLICANT: KIKUCHI, Kaoru
; TITLE OF INVENTION: NOVEL SEMAPHORIN GENE: SEMAPHORIN Y
; FILE REFERENCE: 0020-4527P
; CURRENT APPLICATION NUMBER: US/09/254,594
; CURRENT FILING DATE: 1999-05-11
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 2787
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1..7)
; OTHER INFORMATION: Tissue Type: Brain
; NAME/KEY: CDS
; LOCATION: (1)..(2787)
; OTHER INFORMATION: Identification Method: E
; NAME/KEY: misc feature
; LOCATION: (1)..(1)
; OTHER INFORMATION: Identification Method: P for resulting peptide
US-09-254-594-2

Query Match 2.6%; Score 89.8; DB 4; Length 2787;
Best Local Similarity 50.1%; Pred. No. 1.7e-14;
Matches 369; Conservative 0; Mismatches 347; Indels 21; Gaps 5;

QY 571 AGTGTTCACATTCATCGGTGCTGTTCTTCAATATGTCACCCATCTCTACACCTGCG 630
DB 356 AATGCTACACTACATCCGTGTCTTGTTCCTGGACTCGCAGACACTCTCTGCTGTG 415
QY 631 GCACCTTCGCTTCAGCCCTGCTGTACTCTTCACTTCAAGATTCCTACCTGTTC 690
DB 416 GAACAAATTCCTTCAGCCCTGTGTGTCGACGTATGGGATTAACATCTCTGCAAC----- 469
QY 691 CCATCTCGAGGACAAGTCTATGAGGGAAGGCAAGCCCTTTGACCCCGCTCACA 750
DB 470 -----AGAGGGTGGAGGCTGAGTGGGCAAGCTCGATGCCCTTTGATGCCACCCAGT 523
QY 751 AGCATAGCGTGTCTTGTGATGGGATGCTCTATTCTGTGACTATGAACAATCTCTGG 810
DB 524 CCAGTGTGCCATCTCTCGAGAGGTAGTTTGTACTCAGCCACAGCAGCAGATTTCCAGG 583
QY 811 GCAGTGAAGCCCATCTGATGCGCACACTGGGATCCAGCCTGTCTCTCAAGACCGACAAT 870
DB 584 CCAGTGAAGTGTGTTTACAGAGCCTTGGACCTCAGCCCTCAGCCCTCTCCGTTCTGCAAGT 643
QY 871 TCCTCGGTGGCTGATCATGACGCTCTTGTGGAGGCCAT-----CCCTTCGACCCAGG 927
DB 644 ATGACTTCAAGTGGCTTCGAGAGCCACACTTTGTCTATGCTTTGGAGCATGGAGACCATG 703
QY 928 TCGTCTACTTCTTTCGAGGAGACAGCAGCGAGTTTGACTTTCTTTCGAGAGCTTCCACA 987
DB 704 TCTACTTCTTCTTCGGGAGAACTCTCTGTGAGAGACGCCCGCTCGGGAGGTGCGAT 763
QY 988 CATCGCGGTGCTAGAGTCTCAAGAAATGAGCTGGGCGGCGAAAGCTG-----CTGCAGA 1044
DB 764 TTTCCCGGTGGCCCGGTGTGTAACGCTGATGGTGGCTCACCACCGGCTTTGGATC 823

QY 1045 AGAAGTGAGCACCTTCTGAAGCCAGCTGCTCTGACCCAGCCGGGAGCTGCCCT 1104
DB 824 GCCACTGGACATCTCTCTTAAGCTGAGGCTCAACTGCTCGTCCCTGGGAGCTCTACCT 883
QY 1105 TCACAGTCATCCGACACCGGCTCTGCTCCCGCGGATTTCCACAGCTCCCCACATCT 1164
DB 884 TCTAC-TTTGATGCTTACAGTCTTAACTGGGCTGTGAACCTGCAATGGGCGCTCTGC- 941
QY 1165 AGCAGTCTTCACTCTCCAGTGGCAGGTTGGCGGACCCAGGAGCTCTGCGGTTTGTGCT 1224
DB 942 -CCTCTTTGGGCTCTCACTACTCAGACCAATAGCATTCCTGGTCTGCAGTCTGCGCT 1000
QY 1295 TCTCTCTTGGACATTAAGCTGTCTTAAGGGGAAATACAAAGAGTTGAACAAAGAA 1284
DB 1001 TCTACTAGATGACATTAAGCTGTCTTAAGGGGAAATTTAGGGGAAAGTTCAAGGAGCAGAGGAGTCTGG 1060
QY 1285 CTTACGCTGGACTACT 1301
DB 1061 ATGGGCTTGGACTCT 1077

RESULT 10

US-09-254-594-1

; Sequence 1, Application US/09254594

; Patent No. 6566094

; GENERAL INFORMATION:

; APPLICANT: KIMURA, Toru

; APPLICANT: KIMURA, Kaoru

; TITLE OF INVENTION: NOVEL SEMAPHORIN GENE: SEMAPHORIN Y

; FILE REFERENCE: 0020-4527P

; CURRENT APPLICATION NUMBER: US/09/254,594

; CURRENT FILING DATE: 1998-05-11

; NUMBER OF SEQ ID NOS: 13

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 1

; LENGTH: 3195

; TYPE: DNA

; ORGANISM: Rattus norvegicus

; FEATURE:

; NAME/KEY: misc_feature

; LOCATION: (1)..(50)

; OTHER INFORMATION: Tissue Type: Brain

; NAME/KEY: 5'UTR

; LOCATION: (1)..(50)

; OTHER INFORMATION: Identification Method: E

; NAME/KEY: misc_feature

; LOCATION: (51)..(2837)

; OTHER INFORMATION: CDS; Identification Method: E

; NAME/KEY: 3'UTR

; LOCATION: (2838)..(3195)

; OTHER INFORMATION: Identification Method: E

US-09-254-594-1

Query Match 2.6%; Score 89.8; DB 4; Length 3195;
Best Local Similarity 50.1%; Pred. No. 1.9e-14;
Matches 369; Conservative 0; Mismatches 347; Indels 21; Gaps 5;

QY 571 AGTGTTCACACTTCATCCGTGCTCTGCTTCTTACAAATGTCCACCATCTTACACCTGCG 630
DB 406 AATGCTACAACTACATCCGTGCTTCTTCTCCCTGGAGCTCGCAGACACTCTCTGCTGTG 465
QY 631 GCACCTTCGCTTCAGCCCTGCTTGTACTTCACTTCACTTCACTTCACTTCACTTGTGC 690
DB 466 GAACAAATTCCTTCAGCCCTGCTGTGTCGAGCTATGGGATACATCTCTGCAAC----- 519
QY 691 CCATCTCGGAGGACAGGTCATGGAGGGAAGGCAAGCCCTTTGACCCCGCTCACA 750
DB 520 -----AGAGGGTGAGGAGCTGAGTGGGCAAGCTCGATGCCCTTTTGTATGCCACCCAGT 573
QY 751 AGCATACGGCTGTCTTGGTGGATGGATGCTCTATTCTGTGACTATGAACACTTCTCTGG 810
DB 574 CCACCTGTGGCCATCTCTGACAGAGGGTAGTTTGTACTACGCCACAGCAGAGATTTCCAGG 633

QY 811 GCAGTGAGCCCATCTGATGCGCACACTGGATCCAGCCTGTCTCAAGACCGACAACCT 870
DB 634 CCAGTGATGCTGTGCTTTTACAGAGCCTTGGACCTTCAGCCCCCACTCCGTTCTGCAAGT 693
QY 871 TCCTCCGTGGCTGATCATGACGCTCTTTTGTGGCAGCCAT---CCCTTCGACCCAGG 927
DB 694 ATGACTTCCAGTGGCTTTCAGAGCCACACTTTTGTCTATGCTTTGGAGCATGGAGACCATG 753
QY 928 TCCTTACTTCTTTCGAGGAGACAGCCAGGATTTGAATTTTGTGAGAGGCTCCACA 987
DB 754 TCTACTTCTTCTTCGGAGAAAGTCTCTGTGAGGACGCGCCGCTGGGGAGGGTGCAGT 813
QY 988 CATCGGGGTGCTAGAGTCTCAAGAAATGACGTGGGGGCGGAAAGCTG---CTGCAGA 1044
DB 814 TTTCCGGGTGCGCGGGTGTAAACGTGACATGGTGGCTCACACGGGCTTTGGATC 873
QY 1045 AGAAGTGGACCACTTCTTGAAGGCCAGCTCTGTGACCCAGCCGGGAGCTGCCCT 1104
DB 874 GCCACTGGACATCTTCTTAAAGCTGAGGCTCAACTGTCTCCCTGGGGACTCTACCT 933
QY 1105 TCACGTCTCCGACAGCGGTCCTGCTCCCGCGGATTTCTCCACAGCTCCCCACATCT 1164
DB 934 TCTAC-TTTGATGCTTACAGTCTTAACTGGGCTGTGAACCTGATGGGCGCTCTGC- 991
QY 1165 AGCAGTCTTCACTCCCACTGGGAGTGGCGGACCCAGGAGCTCTGCGGTTTGTGCT 1224
DB 992 -CCTCTTTGGGCTCTTCACTACTCAGACCAATAGCATTCCTGGTCTGCAGTCTGCGCT 1050
QY 1225 TCTCTCTCTTGACATTAAGCTGTCTTTAAGGGGAAATACAAAGAGTTGAACAAAGAA 1284
DB 1051 TCTACCTAGATGACATTAAGCTGTGCTTTGAGGGCAAGTTCAAGGAGCAGAGGAGTCTGG 1110
QY 1285 CTTACGCTGGACTACT 1301
DB 1111 ATGGGCTTGGACTCT 1127

RESULT 11

US-09-976-594-632

; Sequence 632, Application US/09976594

; Patent No. 6673549

; GENERAL INFORMATION:

; APPLICANT: Furness, Michael

; APPLICANT: Buchbinder, Jenny

; TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS

; FILE REFERENCE: PA-0041 US

; CURRENT APPLICATION NUMBER: US/09/976,594

; CURRENT FILING DATE: 2001-10-12

; PRIOR APPLICATION NUMBER: 60/240,409

; PRIOR FILING DATE: 2000-10-12

; NUMBER OF SEQ ID NOS: 1143

; SOFTWARE: PERL Program

; SEQ ID NO 632

; LENGTH: 4286

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: misc_feature

; OTHER INFORMATION: Incyte ID No. 6673549 238322.6

US-09-976-594-632

Query Match 2.4%; Score 84.2; DB 4; Length 4286;
Best Local Similarity 50.3%; Pred. No. 7.8e-13;
Matches 273; Conservative 0; Mismatches 253; Indels 17; Gaps 2;

QY 571 AGTGTTCACACTTCATCCGTGCTCTGCTTCTTACAAATGTCCACCATCTTACACCTGCG 630
DB 611 AGTGTACAACTATATTCTGTTTCTTGTTCCTGGAGCTCCCAAGAGCTCTTGGCTGTG 670
QY 631 GCACCTTCGCTTCAGCCCTGCTTGTACTTCACTTCACTTCAAGATTTCTTACCTGTTC 690
DB 671 GAACGAACCTCATTACGCCCTTGTGCGGAGCTATGGAT-----AACTTCG 718

691 CCATCTCGAGGACAAAGTCATGAGGAGAAAGCCAAAGCCCTTTGACCCGCTCA CA 750
719 TGACAGAGGAGGGGTGAGAACTGAGTGGCAGGCTCGATGCCCTTTGATGCCACCCAGT 778
751 AGCATACGGCTGCTTGGTGGATGCTCTATTCTGTACTATGAACAACCTTCTCTGG 810
779 CCAACGTGGCCATTTTGCAGGGGAGCTGTACTCAGCCACAGCTGGGATTTCCAGG 838
811 GCAGTGAAGCCATCTGATGGGACACTGGGATCCAGCTGTCTTCAAGACCGCAACT 870
839 CCAGTGTGTGTAGTTTACAGAGCCCTTGGGGCCAGCCCACTCCGCTCCGCCAAGT 898
871 TCCTCCGCTGCTCATCATGACGCTCTTTTGGGAGGACATCCCTTCGACCCAGGTG 930
899 ATGACTCAAGTGGCTCGAGAGCCACACTTTGTCCAGGGCTTGGAGCATGGAGCCATG 958
931 TCTACTTCTTCTCGAGAGACAGCCAGCGAGTTTGTCTTTTGGAGAGCTCCACAT 990
959 TCTACTTCTTCTCCGCGAGCTCTCTGTGGAGGATGCTCGGCTGGGAGGGTGCAGTTCT 1018
991 CGCGGTGGCTAGAGTCTGCAAGAAATGACGTGGGCGGCAAAAGCTGTCAGAGA--- 1047
1019 CCCGCTAGCCGAGTATGTAAGTGAATGGGAGCTCGCTTGGGCTGGGAGGGTGCAGTTCT 1078
1048 --AGTGAACCACTTCTGAGAGCCAGCTGCTCTGCAAGCCAGCGGAGCTGCGCTT 1105
1079 CCAGTGGACATCTTCTGAGGCTTGGCTCAAGCTGCTCTGCTGCTGCTGCTGCTGCT 1138
1106 CAA 1108
1139 CTA 1141

RESULT 12

US-08-121-713D-59
; Sequence 59, Application US/08121713D
; Patent No. 5639856
; GENERAL INFORMATION:
; APPLICANT: Goodman, Corey S.
; APPLICANT: Kolodkin, Alex L.
; APPLICANT: Matthes, David
; APPLICANT: Bentley, David R.
; APPLICANT: O'Connor, Timothy
; TITLE OF INVENTION: The Semaphorin Gene Family
; NUMBER OF SEQUENCES: 100
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 Bush Street, Suite 3200
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/121,713D
; FILING DATE: 13-SEP-1993
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Osman, Richard A.
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: B94-002-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 343-4341
; TELEFAX: (415) 343-4342
; TELEX:
; INFORMATION FOR SEQ ID NO: 59:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3560 base pairs
; TYPE: nucleic acid

; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1953
; US-08-121-713D-59

Query Match Similarity 2.2%; Score 78.6; DB 1; Length 3560;
Best Local Similarity 45.2%; Pred. No. 2.5e-11;
Matches 358; Conservative 0; Mismatches 324; Indels 45; Gaps 4;

QY 711 ATGAGGAGAAAGCCAAAGCCCTTTGACCCGCTCAAGCATACGGCTGTCTTGGT 770
Db 139 AAGAACGACAGGCGGTGTGCCCTCAGATCCAGTCAACAACCTCCACTCTGTGCTGCC 198
QY 771 GATGGGATGCTCTATTCTGTGTACTATGAACAACCTTCTTGGGAGTGGAGCCATCTGATG 830
Db 199 GACAAAGAACTGTATTTCGGGTACCGTGGGAGTTTCACTGGCAGCATCGATTATC--- 255
QY 831 CGCACACTGGGATCCAGCCCTGTCTCTCAAGACCGCAAACTTCTCCGCTGGCTGCATCAT 890
Db 256 -----TACCGGGAGCCCTTCAGACCGCAGCATAGCTAAGTCTCAAC 303
QY 891 GACGCTCTCTTTGGGAGCCATCCCTTCGACCCAGCTCGTCTACTTCTTCTTCCAGAG 950
Db 304 GCACCGAACTTTGTGAGCTCATTTACGAGGGGAGCTTTGTCTATTCTTCTTTCGGGAA 363
QY 951 ACAGCCAGCGAGTTTGAATTTCTTTGAGAGGCTCCACACATCGCGGTGGCTAGAGTCTGC 1010
Db 364 ACCGCGGTGTGATTATCACTGTGGCAAGCGATTTATTTCGCGGTTGCCGCTCTGC 423
QY 1011 AAGATGACGTGGGCGGAAAGTCTGTGAGAGAGTGGACCACTTCTTCAAGGCC 1070
Db 424 AAATGGGCAAGAGTGGCGCCGATCGATTCCGCAACCGCTGGACATCTTCTCAAGTCC 483
QY 1071 CAGCTGCTCTGCACCCAGCGGGGAGCTGCGCTTCAACGTCA-----TC 1115
Db 484 CGCTCAACTGCTCTCATTTCCGCGGATTTATCTTTTACTTTAATGAATCCAACTCTGCC 543
QY 1116 CGCCAGCGGCTCTCTCTCCGCGGATTTCTCCAGCTCCGACATACGAGTCTTC 1175
Db 544 AGCAATCTGTGGAGGAGCAGTATGGCTCGATGAGCTCGAAACTGATCTACGGAGTCTTC 603
QY 1176 ACCTCCAGTGGCAGGTTGGGGGACACAGAGGCTCTGCGGTTTGTGCTTCTCTCTTG 1235
Db 604 AACAGCCGAGCAA-----CTCAATTCGCGCTCAGCGGTTTGTGCTTTGCCCTCCAG 657
QY 1236 GACATGAACTGTCTTTAAGGGGAAATACAAAGAGTTGAACAAAGAACTTCAGCTG- 1294
Db 658 GACATTTGCCGATACGTTTGGGGTCAAGGAGCAGCTGGCATCAACTCCAACCTGG 717
QY 1295 -----GACTACTTATAGGGGCGCTGAGACCAACCCCGCCAGGAGTTGCTCAGTG 1346
Db 718 CTGCAGTGAACACGCGCAAGTACCGATCCTCGACCGGTTCTCTGTACAAAGATTCTG 777
QY 1347 GCGCCCTCTCTGATAAGGCGCTGACCTTATGAAGGACCAATTTCTCTGATGATGAGCAA 1406
Db 778 AGAGCGCTTCCGATCCCACTGAACCTTCAAAACACACATTCGCTAATGGAGAGAT 837
QY 1407 GTGGTG 1413
Db 838 GTGCCG 844

RESULT 13

US-08-835-268-59
; Sequence 59, Application US/08835268
; Patent No. 5807826
; GENERAL INFORMATION:
; APPLICANT: Goodman, Corey S.
; APPLICANT: Kolodkin, Alex L.
; APPLICANT: Matthes, David

Query Match	2.2%;	Score 78.6;	DB 1;	Length 3560;	
Best Local Similarity	49.5%;	Pred. No. 2.5e-11;			
Matches 358;	Conservative	0;	Mismatches 324;	Indels 45;	Gaps 4;
QY	711	ATGAGGGAAAAGGCCAAAGCCCTTTGACCCCGCTCACAAAGCATACGGGTCTTGGTG	770		
Db	139	AAGAACGGACAGCGGGTGTCCCTCATGATCCACGTCACAACTCCACCTCTGTGCTGGCC	198		
QY	771	GATGGGATGCTCTATTCTGTGTAATGAACAAATCTCTGGGCGAGTGAGCCATCCCTGATG	830		
Db	199	GACAAAGAACTGATTCCCGGTACCGTGGCGGATTTAGTGGACGCGATCCGATTATC---	255		
QY	831	CGCACACTGGGATCCCAAGCCTGTCTCTCAAGACCGACAAACTTCTCCGCTGGCTGCATCAT	890		
Db	256	-----TACCGGGAGCCCTTCAGACCGAGCAGTACGATAGCCTAAGTCTCAAC	303		
QY	891	GAGCCTCCTTTGTGGCAGCCATCCCTTCGACCCAGGTGCTACTTCTTCTTCGAGGAG	950		
Db	304	GCACCGAACTTTGTGAAGCTCATTTACGCGGGGCACTTTGTCTATTCTTCTTTTCGGGAA	363		
QY	951	ACGCCAGCGAGTTTGACTTCTTTGAGAGGCTCCACACATCGCGGGTGGGTAGAGTCTGC	1010		
Db	364	ACCGCGTTGAGTTTATCACTGTGGCAAGCGATTTATTTCGCGGTTGCCCGGTCTGC	423		
QY	1011	AAGAATGAGTGGCGCGGAAAGACTGCTGCAGAAAGATGGGACCACTTCTCTGAAGGCC	1070		
Db	424	AAATGGGACAAAGGTGGCCCGCATCGATTCCGCAACCGCTGGACATCTTCTCTCAAGTCC	483		
QY	1071	CAGTGTCTCTGACCCAGCGGGGCGAGCTGCGCTTCTCAAGTCA-----TC	1115		

FEATURE: ;
NAME/KEY: CDS ;
LOCATION: 1..1953 ;
US-09-060-692-59 ;

Query Match 2.2%; Score 78.6; DB 2; Length 3560;
Best Local Similarity 49.2%; Pred. No. 2.5e-11;
Matches 358; Conservative 0; Mismatches 324; Indels 45; Gaps 4;

QY 711 ATGAGGAAAGGCGGAAAGCCCTTTGACCCCGCTCACAAGCATACGGCTGTCTGGTG 770
DB |||||
QY 139 AAGAACGACAGGCGGTGTGCCCCCTACGATCCAGTCACAACCTCCAGCTGTGTGGCC 198
DB |||||
QY 771 GATGGATGCTCTATTCTGGTACTATGAACAACCTTCTCGGCGAGTGAGCCCATCTGATG 830
DB |||||
QY 199 GACAACGACTGTATTCGGTACCGTGGCGGATTCAGTGGCAGCATCCGATATC--- 255
DB |||||
QY 831 CGCAGCTGGGATCCAGCCTGTCTCAGACGACCACTTCCTCCGCTGGCTGCATCAT 890
DB |||||
QY 256 -----TACCGGAGCCCTCGACACCGAGTACGATAGCCCTTAAGTCTCAAC 303
DB |||||
QY 891 GACGCTCTTTGCGGACCATCCCTTCGACCCAGGTCTGCTACTTCTCTTCGAGGAG 950
DB |||||
QY 304 GCACGCACTTTGAGCTCATTTACGAGGCGACTTGTCTATTCTTCTTCGGAA 363
DB |||||
QY 951 ACAGCAGCGATTGATCTCTTTGAGAGGCTCCACATCGCGGGTGGCTAGAGTCTGC 1010
DB |||||
QY 364 ACCGCGTGTGATTTATCAACTGTGGCAAGCGATTTATTGCGCGGTGGCCCGCTGC 423
DB |||||
QY 1011 AAGAAATGAGTGGCGGAAAGCTGTGCGAAGAAAGTGAGCACCTTCCTGAGGCG 1070
DB |||||
QY 424 AATGGGACAAGGTGGCCCGCATCGATTCGCAACCGCTGGACATCTTCTCAAGTCC 483
DB |||||
QY 1071 CAGCTGTCTGCACCCAGCGGGGAGCTGCCCTTCAACGTCA-----TC 1115
DB |||||
QY 484 CGCTCAACTGTCTCCATTCGCGGCGATTTATCTTCTACTTTAATGAATCAATCTGCC 543
DB |||||
QY 1116 CGCAGCGGCTCTCTCCCGCGATCTCCACAGCTCCCACTCCAGCTCTTC 1175
DB |||||
QY 544 AGCAATCTGGTGGAGGACAGTATGGCTCGATGAGCTGAACTGATCTACGAGTCTTC 603
QY 1176 ACCTCCAGTGGCAGGTTGGCGGACAGAGCTCTGCGGTTGTGCTTCTCTCTTG 1235
DB |||||
QY 604 AACAGCGCGAGCA-----CTCAATTCGCGCTCAGCGGTTGTGCTTTCGCTCCAG 657
QY 1236 GACATTGACGTCTTTAAGGGGAATACAAGAGTTGACABAGAATCTTCAGCTG- 1294
DB |||||
QY 658 GACATTGCGGATACGTTTGGGTCAGTTCAAGAGCAGACTGGCATCACTCCAACTGG 717
QY 1295 -----GACTACTTATAGGGGCGCTGAGACCAACCCCGCGCAGGCGTGTCTCAGTG 1346
DB |||||
QY 718 CTGCGAGTGAAACAGCCCAAGTACCGATCTCGACCGGTTCTGTCAACAGATTGG 777
QY 1347 GCGCCCTCTGTGATAAGCCCTGACTTCATGAGGACCATTTCTGTATGATGAGCA 1406
DB |||||
QY 778 AGAGCGCTTCGGATCCCACTGAACCTTCATCAAAACACATTCGCTAATGAGAGAT 837
QY 1407 GTGGTG 1413
DB 838 GTGCGG 844

RESULT 15

US-08-833-391-59
; Sequence 59, Application US/08833391
; Patent No. 6013781
; GENERAL INFORMATION:
; APPLICANT: Goodman, Corey S.
; APPLICANT: Kolodkin, Alex L.
; APPLICANT: Matthes, David
; APPLICANT: Bentley, David R.
; APPLICANT: O'Connor, Timothy
; TITLE OF INVENTION: The Semaphorin Gene Family

NUMBER OF SEQUENCES: 100
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
STREET: 268 Bush Street, Suite 3200
CITY: San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/833,391
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/121,713
FILING DATE: 13-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: Osman, Richard A.
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: B94-002-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 343-4341
TELEFAX: (415) 343-4342
TELEX:
INFORMATION FOR SEQ ID NO: 59:
SEQUENCE CHARACTERISTICS:
LENGTH: 3560 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1953
US-08-833-391-59

Query Match 2.2%; Score 78.6; DB 3; Length 3560;
Best Local Similarity 49.2%; Pred. No. 2.5e-11;
Matches 358; Conservative 0; Mismatches 324; Indels 45; Gaps 4;

QY 711 ATGAGGAAAGGCGGAAAGCCCTTTGACCCCGCTCACAAGCATACGGCTGTCTGGTG 770
DB |||||
QY 139 AAGAACGACAGGCGGTGTGCCCCCTACGATCCAGTCACAACCTCCAGCTGTGTGGCC 198
DB |||||
QY 771 GATGGATGCTCTATTCTGGTACTATGAACAACCTTCTCGGCGAGTGAGCCCATCTGATG 830
DB |||||
QY 199 GACAACGAACTGTATTCGGTACCGTGGCGGATTTTCAGTGGCAGCATCCGATATC--- 255
DB |||||
QY 831 CGCAGCTGGGATCCAGCCTGTCTCAAGACCGCAACTTCTCCGCTGGCTGCATCAT 890
DB |||||
QY 256 -----TACCGGAGCCCTCGACACCGAGTACGATAGCCCTTAAGTCTCAAC 303
DB |||||
QY 891 GACGCTCTTTGTCGACGCATCCCTTCGACCGAGCTGTCTACTTCTTTCGAGGAG 950
DB |||||
QY 304 GCACCGAACTTTGTGAGCTCATTTACGAGGCGGACTTTGTCTATTCTTCTTCGGAA 363
DB |||||
QY 951 ACAGCCAGCGAGTTTGACTTCTTTGAGAGGCTCCACATCGCGGGTGGCTAGAGTCTGC 1010
DB |||||
QY 364 ACCGCGTGTGAGTTTATCAACTGTGCAAGGCGATTTATTTCGGCGTTCGCCGCTGC 423
DB |||||
QY 1011 AAGAAATGAGTGGCGGCGGAAAGCTGTGCGAAGAAAGTGAGCACCTTCCTGAGGCG 1070
DB |||||
QY 424 AATGGGACAAGGTGGCCCGCATCGATTCGCAACCGCTGGACATCTTCTCAAGTCC 483
DB |||||
QY 1071 CAGCTGTCTGCACCCAGCGGGGAGCTGCCCTTCAACGTCA-----TC 1115
DB |||||
QY 484 CGCTCAACTGTCTCCATTCGCGGCGATTTATCTTCTACTTTAATGAATCAATCTGCC 543
DB |||||
QY 1116 CGCAGCGGCTCTCTCCCGCGATCTCCACAGCTCCCACTCCAGCTCTTC 1175

Db	544	AGCAATCTGGTGGAGGACAGTATGGCTCGATGAGCTCGAAACTGATCTACGGAGTCTTC	603
Qy	1176	ACCTCCCAAGTGGCAGGTTGGCGGACAGGAGCTCTGGGTTTGTGCTTCTCTCTCTG	1235
Db	604	AACAGCCCGAGCAA-----CTCAATCCCGCTCAGCGGTTGTGCTTGGCCCTCCAG	657
Qy	1236	GACATTGAACGTGTCTTTAAGGGGAAATACAAAGAGTTGAACAAAGAACTTCACGCTG-	1294
Db	658	GACATTGCCGATACCGTTTGAAGGTCAGTTCAAGGAGCAGACTGGCATCAACTCCAACTGG	717
Qy	1295	-----GACTACTTATAGGGCCCTGAGACCAACCCCGCCAGGCAAGTGTCTCAGTG	1346
Db	718	CTGCCAGTGAACAACGCCAAGTACCCGATCTCGACCCGGTTCTGTCAACAGATTCTG	777
Qy	1347	GGCCCCCTCTCTGATAAGGCCCTGACCTTTCATGAAGGACCAATTCCTGATCGATGAGCAA	1406
Db	778	AGAGCGCTTCGGATCCCACTGAACTTCATCAAAACACATTCGCTAATGGAGGAGAAAT	837
Qy	1407	GTGGTGG	1413
Db	838	GTGCCGG	844

Search completed: April 26, 2004, 02:10:54
Job time : 180.879 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: April 24, 2004, 23:47:42 ; Search time 931.295 Seconds

(without alignments)
15988.422 Million cell updates/sec

Title: US-10-051-835-13

Perfect score: 3505

Sequence: 1 ggcttgccatgatgggac.....tttgggccaaccacaggttg 3505

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 337363 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N_Geneseq_29Jan04:*

1: Geneseq1980s:*

2: Geneseq1990s:*

3: Geneseq2000s:*

4: Geneseq2001as:*

5: Geneseq2001bs:*

6: Geneseq2002s:*

7: Geneseq2003as:*

8: Geneseq2003bs:*

9: Geneseq2003cs:*

10: Geneseq2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	3060.8	87.3	3143	3 AAC58392	Human PRO
2	3060.8	87.3	3143	8 ACD68436	Novel hum
3	3060.8	87.3	3143	8 ACD68436	Novel hum
4	3060.8	87.3	3143	8 ACD68436	Novel hum
5	3060.8	87.3	3143	9 ACD68082	Novel hum
6	3060.8	87.3	3143	9 ACD68082	Novel hum
7	3060.8	87.3	3143	9 ACD68082	Novel hum
8	3060.8	87.3	3143	9 ACD68082	Novel hum
9	3060.8	87.3	3143	9 ACD68082	Novel hum
10	3060.8	87.3	3143	9 ACD68082	Novel hum
11	3060.8	87.3	3143	9 ACD68082	Novel hum
12	3060.8	87.3	3143	9 ACD68082	Novel hum
13	3060.8	87.3	3143	9 ACD68082	Novel hum
14	3060.8	87.3	3143	9 ACD68082	Novel hum
15	3060.8	87.3	3143	9 ACD68082	Novel hum
16	3060.8	87.3	3143	9 ACD68082	Novel hum
17	3060.8	87.3	3143	9 ACD68082	Novel hum
18	3060.8	87.3	3143	9 ACD68082	Novel hum
19	3060.8	87.3	3143	9 ACD68082	Novel hum
20	3060.8	87.3	3143	9 ACD68082	Novel hum
21	3060.8	87.3	3143	9 ACD68082	Novel hum
22	3060.8	87.3	3143	9 ACD68082	Novel hum
23	3060.8	87.3	3143	9 ACD68082	Novel hum

24	3031.4	86.5	3191	3 AAC69084	Human sec
25	3022.4	86.2	3146	7 ACC69002	Human neu
26	2998.8	85.6	3075	4 AAF54397	DNA encod
27	2682.2	76.5	2981	9 ADB62165	Human CDN
28	2642.8	75.4	2768	6 ABS64946	Human CDN
29	2435.4	69.5	2745	7 ACC68985	Human neu
30	2381.4	65.1	2283	5 AAF45126	Human TAN
31	2281.4	65.1	2283	7 ACD68781	Secreted
32	2279.4	65.0	2281	6 AAD28945	Human MOL
33	2279.4	65.0	2281	6 AAD28945	Human MOL
34	2226.8	63.5	2271	6 AAD28944	Human MOL
35	2226.8	63.5	2271	6 AAD28944	Human MOL
36	2114.4	60.3	2238	7 ACC69003	Human neu
37	1858	52.4	1838	4 AAH15636	Human CDN
38	1726.8	49.3	3046	5 AAF45137	Murine se
39	1726.8	49.3	3046	5 AAF45137	Murine DN
40	1726.8	49.3	3046	5 AAF45137	Murine DN
41	1726.8	49.3	3046	7 ACD26370	Secreted
42	1708.8	48.8	1901	4 AAK53434	Human pol
43	1197.8	33.9	1674	6 ABK94920	Human nov
44	918.4	26.2	1730	6 ABS54021	CDNA enco
45	698.2	19.9	775	4 AAH04875	Human CDN

ALIGNMENTS

RESULT 1
AAC58392
ID AAC58392 standard; cDNA; 3143 BP.
XX
AC AAC58392;
XX
DT 29-JAN-2001 (first entry)
XX
DE Human PRO1317 nucleotide sequence SEQ ID NO:70.
XX
KW Human; tumour; diagnosis; neoplastic disease; neoplastic cell growth;
KW proliferation; tumorigenesis; identification; cancer; cytostatic;
KW notoprotective; antiinflammatory; immunosuppressive;
KW immunostimulant; antiangiogenic; leukaemia; lymphoid malignancy;
KW neuronal disorder; glioma; astrocytic disorder; angiogenic;
KW hypothalamic disorder; glandular disorder; macrophagal disorder;
KW epithelial disorder; surmal disorder; blastocoelec disorder;
KW inflammatory disorder; immunologic disorder; ss.
XX
OS Homo sapiens.
XX
PN WO200053755-A2.
XX
PD 14-SEP-2000.
XX
PF 06-JAN-2000; 2000WO-US000376.
XX
PR 08-MAR-1999; 99WO-US005028.
PR 02-JUN-1999; 99WO-US012252.
PR 23-JUN-1999; 99US-0141037P.
PR 07-JUL-1999; 99US-0143048P.
PR 26-JUL-1999; 99US-0145698P.
PR 30-NOV-1999; 99WO-US028313.
PR 20-DEC-1999; 99WO-US030911.
PR 05-JAN-2000; 2000WO-US000219.
XX
(GETH) GENENTECH INC.
XX
PI Ashkenazi AJ, Baker KP, Goddard A, Gurney AL, Hillan KJ, Roy MA;
PI Watanabe CK, Wood WT;
XX
DR WPI; 2000-572270/53.
DR P-PSDB; AAE24084.
XX
PT Thirty PRO polynucleotides encoding PRO polypeptides, useful in the
PT treatment, diagnosis and prevention of cancer.

XX PS Claim 50; Fig 51; 286pp; English.

XX CC The present invention describes an isolated antibody that binds to one of

CC the human PRO proteins designated PRO212, PRO290, PRO341, PRO535, PRO619,

CC PRO717, PRO809, PRO830, PRO848, PRO943, PRO1005, PRO1009, PRO1025,

CC PRO1030, PRO1097, PRO1107, PRO1111, PRO1153, PRO1182, PRO1184, PRO1187,

CC PRO1281, PRO23, PRO39, PRO334, PRO1317, PRO1710, PRO2094, PRO2145 OR

CC PRO2198. PRO antagonists can be used to inhibit tumour cell growth. The

CC PRO polypeptides and nucleotides are useful in the treatment, diagnosis

CC and prevention of cancer. The antibodies and other anti-tumour compounds

CC may be used to treat various conditions, including those characterised by

CC overexpression and/or activation of the amplified PRO genes. Exemplary

CC conditions or disorders to be treated with such antibodies and other

CC compounds include benign or malignant tumours (e.g., renal, liver,

CC kidney, bladder, breast, gastric, ovarian, colorectal, prostate,

CC pancreatic, lung, vulva, thyroid, hepatic carcinomas, sarcomas and

CC glioblastomas, and various head and neck tumours), leukaemias and

CC lymphoid malignancies, other disorders such as neuronal, glial,

CC astrocytic, hypothalamic and other glandular, macrophagal, epithelial,

CC stromal and blastocoeleic disorders, and inflammatory, angiogenic and

CC immunologic disorders. AAC58242 to AAC58366 represent PCR primers and

CC hybridisation probes used in the isolation of the human PRO sequences.

CC AAC58367 to AAC58396 and AAB24037 to AAB24089 represent human PRO

CC polynucleotide and protein sequences given in the exemplification of the

CC present invention

XX SQ Sequence 3143 BP; 656 A; 963 C; 828 G; 696 T; 0 U; 0 Other;

Query Match 87.3%; Score 3060.8; DB 3; Length 3143;

Best Local Similarity 99.9%; Pred. No. 0;

Matches 3062; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 173 AGAGTCCCTGGTGAAGTCTGTGGTGTAGCATGGCCCTCCAGCCCTGGGCTGGACCC 232

DB 74 AGAGTCCCTGGTGAAGTCTGTGGTGTAGCATGGCCCTCCAGCCCTGGGCTGGACCC 133

QY 233 CTGGAGCTCTGGGCTTTCTCTTCCAACTGCTTCAGTCTGCTGCTGCCGACGACGAC 292

DB 134 CTGGAGCTCTGGGCTTTCTCTTCCAACTGCTTCAGTCTGCTGCTGCCGACGACGAC 193

QY 293 CGCGGGGGAGGGGGAGGGGGCCCATGCGCCAGGGTCAATATGACAGGGGATGAAGC 352

DB 194 CGCGGGGGAGGGGGAGGGGGCCCATGCGCCAGGGTCAATATGACAGGGGATGAAGC 253

QY 353 TAGGGCACTTAGCTTCTTCCAGAGAGGGCTCCAGGATTTTGACACTTCTGCTCTGAG 412

DB 254 TAGGGCACTTAGCTTCTTCCAGAGAGGGCTCCAGGATTTTGACACTTCTGCTCTGAG 313

QY 413 TGGTGTGGAATTAATCTCTACCTGGGGCTCGAGAAGCCATTTCTGGCTTGGATATCCA 472

DB 314 TGGTGTGGAATTAATCTCTACCTGGGGCTCGAGAAGCCATTTCTGGCTTGGATATCCA 373

QY 473 GGATCCAGGGGTCCCGAGGTCAAGACATGATACCGTGGCCAGCCAGTGAAGAAAAA 532

DB 374 GGATCCAGGGGTCCCGAGGTCAAGACATGATACCGTGGCCAGCCAGTGAAGAAAAA 433

QY 533 GAGTGAATGTGCCCTTTAAGAGAGAGCAATGAGACACAGTGTTCATCTTCCTGCT 592

DB 434 GAGTGAATGTGCCCTTTAAGAGAGAGCAATGAGACACAGTGTTCATCTTCCTGCT 493

QY 593 CTGGTGTCTTCAATGTACCAATCTTACACCTGGGACCTTCGCTTCAGCCCTGC 652

DB 494 CTGGTGTCTTCAATGTACCAATCTTACACCTGGGACCTTCGCTTCAGCCCTGC 553

QY 653 TTGTACCTTCAATGAATCTCAAGATTCCTACCTGTGTTGCCATCTCGAGGACAGGTAT 712

DB 554 TTGTACCTTCAATGAATCTCAAGATTCCTACCTGTGTTGCCATCTCGAGGACAGGTAT 613

QY 713 GGAGGGAAAAAGGCCAAAGCCCTTTGACCCCGCTCAAGACATACGGCTGTCTTGTGGA 772

DB 614 GGAGGGAAAAAGGCCAAAGCCCTTTGACCCCGCTCAAGACATACGGCTGTCTTGTGGA 673

QY 773 TGGATGCTCTATTCTGTTACTATGAACAACCTTCTCGGCACTGAGCCCATCTGATGGC 832

DB 674 TGGATGCTCTATTCTGTTACTATGAACAACCTTCTCGGCACTGAGCCCATCTGATGGC 733

QY 833 CACACTGGGATCCCGAGCTGTCTCTCAAGACCGCAACTTCTCGCTGGTGGCATCATGA 892

DB 734 CACACTGGGATCCCGAGCTGTCTCTCAAGACCGCAACTTCTCGCTGGTGGCATCATGA 793

QY 893 CGCTCTCTTTGTGGCAGCATCTCTTCGACCCAGGTGCTTACTTCTTCTCGAGGAGAC 952

DB 794 CGCTCTCTTTGTGGCAGCATCTCTTCGACCCAGGTGCTTACTTCTTCTCGAGGAGAC 853

QY 953 AGCCAGCGAGTTTACACTTCTTTAGAGGCTCCACACATCGGGGTGCTAGAGTCTCAA 1012

DB 854 AGCCAGCGAGTTTACACTTCTTTAGAGGCTCCACACATCGGGGTGCTAGAGTCTCAA 913

QY 1013 GAATGACGTGGGGCGGCAAAAGCTGTCTGAGAGAGTGGACACACCTTCTGAGGGCCCA 1072

DB 914 GAATGACGTGGGGCGGCAAAAGCTGTCTGAGAGAGTGGACACACCTTCTGAGGGCCCA 973

QY 1073 GCTGCTCTGACCCAGCGGGGAGCTGCCCTTCAAGCTCATCGCCACCGCTCTGCT 1132

DB 974 GCTGCTCTGACCCAGCGGGGAGCTGCCCTTCAAGCTCATCGCCACCGCTCTGCT 1033

QY 1133 CCCGCGCATTTCTCCACAGCTCCCACTACGAGTCTTCACTTCCAGTGGGAGGT 1192

DB 1034 CCCGCGCATTTCTCCACAGCTCCCACTACGAGTCTTCACTTCCAGTGGGAGGT 1093

QY 1193 TGGGGGACACAGGAGCTCTGGGTTTGTGCTTCTCTCTGAGACATTCGAGTGTCT 1252

DB 1094 TGGGGGACACAGGAGCTCTGGGTTTGTGCTTCTCTCTCTGAGACATTCGAGTGTCT 1153

QY 1253 TAAGGGGAAATPACAAAGAGTTGAACAAAGAACTTCACTGCTGAGTACTTATAGGGGCC 1312

DB 1154 TAAGGGGAAATPACAAAGAGTTGAACAAAGAACTTCACTGCTGAGTACTTATAGGGGCC 1213

QY 1313 TGAGACCAACCCCGGGCAGGAGTGTCTCAGTGGGGCCCTCTCTCTATAGGCCCTGAC 1372

DB 1214 TGAGACCAACCCCGGGCAGGAGTGTCTCAGTGGGGCCCTCTCTCTATAGGCCCTGAC 1273

QY 1373 CTTTATGAAGACCATTTTCTGATGAGTGAAGTGGTGGGACGCGCCCTGCTGTGTGAA 1432

DB 1274 CTTTATGAAGACCATTTTCTGATGAGTGAAGTGGTGGGACGCGCCCTGCTGTGTGAA 1333

QY 1433 ATCTGGGGTGGAGTATACAGGCTTGCAGTGGAGACAGCCAGGCTTGTATGGGACAG 1492

DB 1334 ATCTGGGGTGGAGTATACAGGCTTGCAGTGGAGACAGCCAGGCTTGTATGGGACAG 1393

QY 1493 CCATCTTGTCTATGTACCTGGGAACCAACACAGGGTCTCTCCAAAGGCTGTGTAAGTGG 1552

DB 1394 CCATCTTGTCTATGTACCTGGGAACCAACACAGGGTCTCTCCAAAGGCTGTGTAAGTGG 1453

QY 1553 GGACAGAGTGTCTATCTGTTGGAGAGATTCAGTGTTCCTGTGACCTGAACTGTCTG 1612

DB 1454 GGACAGAGTGTCTATCTGTTGGAGAGATTCAGTGTTCCTGTGACCTGAACTGTCTG 1513

QY 1613 CAACCTGAGTGTGCCCCCAGGCTGAGTGTGTTGTAGGTTTCTCAGAGGTGTCTG 1672

DB 1514 CAACCTGAGTGTGCCCCCAGGCTGAGTGTGTTGTAGGTTTCTCAGAGGTGTCTG 1573

QY 1673 GAGGGTCCCGGAGCCAACTGTGTATGAGAGTGTGTGAGTGTGTCTTGTGCCCCG 1732

DB 1574 GAGGGTCCCGGAGCCAACTGTGTATGAGAGTGTGTGAGTGTGTCTTGTGCCCCG 1633

QY 1733 GGACCCCACTGTGCTCGGACCTGAGTCCCGAACCTGTTGCTCTGCTGTGCCCCCA 1792

DB 1634 GGACCCCACTGTGCTCGGACCTGAGTCCCGAACCTGTTGCTCTGCTGTGCCCCCA 1693

QY 1793 CCTGAACTCTGGAAGCAGACATGGAGCGGGGAAACCCAGAGTGGGCACTGTGCCAGTGG 1852

DB 1694 CCTGAACTCTGGAAGCAGACATGGAGCGGGGAAACCCAGAGTGGGCACTGTGCCAGTGG 1753

QY 1853 CCCCATGAGCAGGAGCCTTCGGCTCAGAGCCCGCCCAATCATTAAGAAAGTCTCTGGC 1912

Db	1754	CCCCATGAGCAGGAGCCTTTGGCCCTCAGAGCGCCGCAATCATTAAGAAAGTCTGGC	1813
Qy	1913	TGTCCCTPAACTCATCTGGAGTCCCTGCCCCACACTGTGAGCTTGGCCTCTATTATA	1972
Db	1814	TGTCCCAACTCATCTGGAGTCCCTGCCCCACACTGTGAGCTTGGCCTCTATTATA	1873
Qy	1973	TTGGAGTCATGGCCCCAGCAGCAGTCCAGAAAGCCTTTCACACTGTCTACAATGGTCCCT	2032
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Qy	2033	CTTGCTGATAGTCCAGATGGAGTTGGGGTCTCTACCAAGTCTTGGGCAACTTGAGATGG	2092
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Qy	2093	CTTTTTCATACCTGTGTATCTCTACTTGGGTGGACAGCAGGACACAGACCTTGGCCCTGA	2152
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Qy	2153	TCTTGAACTGGCAGGCAATCCCCGGGAGCATGTGAAGTCCCTTGAACAGGTCAGTGG	2212
Db	2054	TCTTGAACTGGCAGGCAATCCCCGGGAGCATGTGAAGTCCCTTGAACAGGTCAGTGG	2113
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Qy	2273	CTTTGGCCTTAGTCTTTTCAGGAGCCCTCATCATCTCTGTGGCCCTCCCCATTTGAGAGCACT	2332
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8436 ACD68436 standard: cDNA: 3143 BP.

ACD68436;

17-SEP-2003 (first entry)

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Homo sapiens.

US2003073130-A1.

17-APR-2003.

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(GETH) GENENTECH INC.

Baker KD, Botstein D, Desnoyers L, Eaton DL, Ferrara N, Fong S;
Gao W, Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillian KJ;
Pan J, Paoni NF, Roy MA, Smith V, Stewart TA, Tumas D, Watanabe CK;
Williams PM, Wood WL;


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DT 01-OCT-2003 (first entry)
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cardiant; antidiabetic; anorectic; antiarthritic; angiogenesis; cancer;
adrenal cortical capillary; endothelial cell growth; wound healing;
stimulated T-lymphocyte proliferation; immune response suppression;
neonatal heart hypertrophy; cardiac insufficiency disorder;
vascular endothelial growth factor; inflammation; mononuclear cell;
eosinophil; diabetes; obesity; or hyper-insulinaemia; hypo-insulinaemia;
chondrocyte redifferentiation; bone disorder; cartilage disorder;
sports injury; arthritis.
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XX
PN US2003044841-A1.
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PD 06-MAR-2003.
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PF 06-DEC-2001; 2001US-00006856.
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PR	28-OCT-1998;	98US-0106032P.	PR		
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PR	03-NOV-1998;	98US-01069			

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RESULT 4
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17-SEP-2003 (first entry)
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XX tissue typing; chromosome identification; vaccine; gene; ss.
XX Homo sapiens.
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PN US2003073129-A1.
XX
PD
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XX
PF 04-SEP-2001; 2001US-00946374.
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PR 08-OCT-1998; 98US-0103679P.
PR 08-OCT-1998; 98US-0103711P.
PR 14-OCT-1998; 98US-0104257P.
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PR 21-OCT-1998; 98US-0105104P.
PR 22-OCT-1998; 98US-0105169P.
PR 22-OCT-1998; 98US-0105266P.
PR 26-OCT-1998; 98US-0105693P.
PR 26-OCT-1998; 98US-0105694P.
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PR 03-NOV-1998; 98US-0106932P.
PR 03-NOV-1998; 98US-0106934P.
PR 10-NOV-1998; 98US-0107783P.
PR 17-NOV-1998; 98US-0108775P.
PR 17-NOV-1998; 98US-0108779P.
PR 17-NOV-1998; 98US-0108787P.
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PR 17-NOV-1998; 98US-0108867P.
PR 17-NOV-1998; 98US-0108925P.
PR 18-NOV-1998; 98US-0108848P.
PR 18-NOV-1998; 98US-0108849P.
PR 18-NOV-1998; 98US-0108850P.
PR 18-NOV-1998; 98US-0108851P.
PR 18-NOV-1998; 98US-0108852P.
PR 18-NOV-1998; 98US-0108858P.
PR 18-NOV-1998; 98US-0108904P.
PR 22-DEC-1998; 98US-0021851P.
PR 22-DEC-1998; 98US-0113296P.
PR 30-DEC-1998; 98US-0114223P.
PR 05-JAN-1999; 98US-0000106.
PR 12-APR-1999; 98US-0028429P.
PR 16-APR-1999; 98US-0129674P.
PR 23-JUN-1999; 98US-0141037P.
PR 26-JUL-1999; 98US-0144758P.
PR 01-SEP-1999; 98US-0145698P.
PR 15-SEP-1999; 98US-0020111.
PR 18-OCT-1999; 98US-0040329P.
PR 30-NOV-1999; 98US-0028313.
PR 02-DEC-1999; 98US-0028551.
PR 16-DEC-1999; 98US-0030095.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004342.
PR 24-FEB-2000; 2000WO-US005004.
PR 02-MAR-2000; 2000WO-US005841.
PR 15-MAR-2000; 2000WO-US006884.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015244.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 08-NOV-2000; 2000WO-US030952.
PR 10-NOV-2000; 2000WO-US030873.
PR 01-DEC-2000; 2000WO-US032678.
PR 28-FEB-2001; 2001WO-US006520.
PR 01-MAR-2001; 2001WO-US006666.
PR 01-JUN-2001; 2001US-00872035.
PR 01-JUN-2001; 2001WO-US017800.
PR 14-JUN-2001; 2001US-00882636.
PR 20-JUN-2001; 2001WO-US019692.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
XX
XX (GETH ) GENENTECH INC.
XX
XX Baker KP, Botstein D, Desnoyers L, Eaton DL, Ferrara N, Fong S;
XX Gao W, Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ;
XX Fan J, Paoni NF, Roy MA, Smith V, Stewart TA, Tumas D, Watanabe CK;
XX Williams PM, Wood WI;
XX
XX WBI: 2003-585292/55.
XX P-PSDB; ABO33537.
XX
XX Novel isolated PRO polypeptides e.g. PRO1491 and PRO1571, useful in the
XX preparation of a medicament for treating a condition responsive to PRO
XX polypeptide, and as therapeutic agents e.g. vaccines.
XX
XX Claim 2; Fig 157; 561pp; English.
XX
XX The invention describes an isolated PRO (secreted and transmembrane)
XX polypeptide (1), having at least 80% sequence identity to a sequence
XX
Query Match 87.3%; Score 3060.8; DB 8; Length 3143;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 3062; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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DB 74 AGAGCTCCCTGGTGACAGCTCTGGCTGAGCATGCGCTCCAGCATGCGCTCCAGCGCTGGGCGCTGGAGCC 133
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Qy	773	TGGGATGCTCTATTCTGTGTAATATGAACAACTTCTGGGAGTGAAGCCATCTCTGATGCG	832
Db	674	TGGGATGCTCTATTCTGTGTAATATGAACAACTTCTGGGAGTGAAGCCATCTCTGATGCG	733
Qy	833	CACACTGGATCCGAGCCCTGCTCAAGACCGACAACTTCTCCGCTGGCTGCTCATGA	892
Db	734	CACACTGGATCCGAGCCCTGCTCAAGACCGACAACTTCTCCGCTGGCTGCTCATGA	793
Qy	893	CGCTCTCTTTGTGGCAGCATCCCTTCGACCCAGTGTCTTCTTCTTCTGAGGAGAC	952
Db	794	CGCTCTCTTTGTGGCAGCATCCCTTCGACCCAGTGTCTTCTTCTTCTTCTGAGGAGAC	853
Qy	953	AGCCAGCGAGTTGACTTCTTTGAGAGCTCCACACATCGCGGTGGCTAGGTCGCA	1012
Db	854	AGCCAGCGAGTTGACTTCTTTGAGAGCTCCACACATCGCGGTGGCTAGGTCGCA	913
Qy	1013	GAAAGACCTGGCGCGGAAAGCTGCTCAGAGAGTGAACCACTTCTTGAAGGCCA	1072
Db	914	GAAAGACCTGGCGCGGAAAGCTGCTCAGAGAGTGAACCACTTCTTGAAGGCCA	973
Qy	1073	GCTGCTCTGACCCAGCGCGGAGCTGCTGCCCTTCAACGTCTATCCGCCACGCGTCTGCT	1132
Db	974	GCTGCTCTGACCCAGCGCGGAGCTGCTGCCCTTCAACGTCTATCCGCCACGCGTCTGCT	1033
Qy	1133	CCCCCGCATTTCTCCACAGTCCCCACATCTAGCAGTCTTCACTCCACAGTGGCAGGT	1192
Db	1034	CCCCCGCATTTCTCCACAGTCCCCACATCTAGCAGTCTTCACTCCACAGTGGCAGGT	1093
Qy	1193	TGGCGGACACAGGAGCTCTGCGGTTTGTGCTTCTCTCTTGGACATTTGAACGTGCTT	1252
Db	1094	TGGCGGACACAGGAGCTCTGCGGTTTGTGCTTCTCTCTTGGACATTTGAACGTGCTT	1153
Qy	1253	TAAAGGGAATACAAAGAGTTGAACAAAGAACTTCACGCTGGACTATTATAGGCGCC	1312
Db	1154	TAAAGGGAATACAAAGAGTTGAACAAAGAACTTCACGCTGGACTATTATAGGCGCC	1213
Qy	1313	TGAGACCAACCCCGCCAGCGAGTTGCTCAGTGGGCGCCCTCTCTGATAGGCGCTGAC	1372
Db	1214	TGAGACCAACCCCGCCAGCGAGTTGCTCAGTGGGCGCCCTCTCTGATAGGCGCTGAC	1273
Qy	1373	CTTCATGAAGGACCAATTTCTGATGGATGAGCAAGTGTGGGAGCGCCCTGCTGGTGAA	1432
Db	1274	CTTCATGAAGGACCAATTTCTGATGGATGAGCAAGTGTGGGAGCGCCCTGCTGGTGAA	1333
Qy	1433	ATCTGGCTGGAGTATACAGGCTTGCAGTGGAGACAGCCAGGCGCTTGTATGGGCACAG	1492
Db	1334	ATCTGGCTGGAGTATACAGGCTTGCAGTGGAGACAGCCAGGCGCTTGTATGGGCACAG	1393
Qy	1493	CAATCTGTATGTACCTTGGGAACCAACAGGCTGCTTCAAGAGCTGTGGTAAGTGG	1552
Db	1394	CAATCTGTATGTACCTTGGGAACCAACAGGCTGCTTCAAGAGCTGTGGTAAGTGG	1453
Qy	1553	GGACAGAGTGTCTATCTGTGGAGAGATTACAGTGTCTTCCCTGACCTGAACCTGTTCG	1612
Db	1454	GGACAGAGTGTCTATCTGTGGAGAGATTACAGTGTCTTCCCTGACCTGAACCTGTTCG	1513
Qy	1613	CAACCTGACGTGGCCCCCACCAGGCTGAGTGTCTTGTAGGCTTCTCAGAGGTGTCTG	1672
Db	1514	CAACCTGACGTGGCCCCCACCAGGCTGAGTGTCTTGTAGGCTTCTCAGAGGTGTCTG	1573
Qy	1673	GAGGCTCCCGAGCCAACTGTAGTGTCTATGAGAGCTGTGGAGCTGTGCTTGGCCG	1732
Db	1574	GAGGCTCCCGAGCCAACTGTAGTGTCTATGAGAGCTGTGTGGAGCTGTGCTTGGCCG	1633
Qy	1733	GGACCCCACTGTGCTGGAGCCCTGAGTCCGGAACCTGTGCTCTCTGCTGCCCCCAA	1792

Db	1634	GGACCCCACTGTGCTGGGACCTTGAGTCCCGAACCTGTGCTCTCTCTGCCCCCAA	1693
Qy	1793	CTTGAACCTCTCGAAGACGACATCGAGCGGGGAACCCAGAGTGGCATGTGCCAGTGG	1852
Db	1694	CTTGAACCTCTCGAAGACGACATCGAGCGGGGAACCCAGAGTGGCATGTGCCAGTGG	1753
Qy	1853	CCCCATGACGAGGAGCCTTGGCCCTCAGAGCGCGCCGCAAAATCATTAAGAAAGTCTTGGC	1912
Db	1754	CCCCATGACGAGGAGCCTTGGCCCTCAGAGCGCGCCGCAAAATCATTAAGAAAGTCTTGGC	1813
Qy	1913	TGTCCCTAATCCATCTCGAGCTCCCTGCGCCCACTGTCTCAGCTTGGCCCTCTTATTA	1972
Db	1814	TGTCCCAACTCCATCTCGAGCTCCCTGCGCCCACTGTCTCAGCTTGGCCCTCTTATTA	1873
Qy	1973	TTGGAGTCTATGCCCCCAGCAGCAGTCTTCCAGAGCTCTTCCACTGTCTCAATGGCTCCCT	2032
Db	1874	TTGGAGTCTATGCCCCCAGCAGCAGTCTTCCAGAGCTCTTCCACTGTCTCAATGGCTCCCT	1933
Qy	2033	CTTGTCTAGTGCAGGATGGAGTTGGGGTCTCTACAGTGTCTGCGCAACTGAGAAATGG	2092
Db	1934	CTTGTCTAGTGCAGGATGGAGTTGGGGTCTCTACAGTGTCTGCGCAACTGAGAAATGG	1993
Qy	2093	CTTTTTCATACCTGTGATCTCTTACTTGGGTGACAGCCAGGACCCCTGGCCCTGGA	2152
Db	1994	CTTTTTCATACCTGTGATCTCTTACTTGGGTGACAGCCAGGACCCCTGGCCCTGGA	2053
Qy	2153	TCCTGMACTGGCAGGCAATCCCGGAGCATGTGAAGTCCCGTTGACAGAGGTCACTGG	2212
Db	2054	TCCTGMACTGGCAGGCAATCCCGGAGCATGTGAAGTCCCGTTGACAGAGGTCACTGG	2113
Qy	2213	TGGGGCGCCCTGGCTGCCCCAGCAGTCTCTACTTGGCCCCCACTTTGTCACTGTCTCT	2272
Db	2114	TGGGGCGCCCTGGCTGCCCCAGCAGTCTCTACTTGGCCCCCACTTTGTCACTGTCTCT	2173
Qy	2273	CTTTGCTTGTAGTCTTTTCAAGAGCCCTCATCATCTCTGCGCCCTCCCCATTTGAGAGCACT	2332
Db	2174	CTTTGCTTGTAGTCTTTTCAAGAGCCCTCATCATCTCTGCGCCCTCCCCATTTGAGAGCACT	2233
Qy	2333	CGGGCTCGGGCAAGTTTCAAGAGCCCTCATCATCTCTGCGCCCTCCCCATTTGAGAGCACT	2392
Db	2234	CGGGCTCGGGCAAGTTTCAAGAGCCCTCATCATCTCTGCGCCCTCCCCATTTGAGAGCACT	2293
Qy	2393	AAGCAGAGCAACACCTCCAGTCTCTCCAAAGAAATGACAGGACCTCTGCGAGTGTGGA	2452
Db	2294	AAGCAGAGCAACACCTCCAGTCTCTCCAAAGAAATGACAGGACCTCTGCGAGTGTGGA	2353
Qy	2453	CGCTGACAACTAGCTAGGCACTGAGTGTCTTAACTCTAGCAGACAGGCGCGGCTG	2512
Db	2354	CGCTGACAACTAGCTAGGCACTGAGTGTCTTAACTCTAGCAGACAGGCGCGGCTG	2413
Qy	2513	CGGTGAGGCACTGCGCATGCTGGCGCGGCCCAAGCAGAGCCCTGACTAGGATGAC	2572
Db	2414	CGGTGAGGCACTGCGCATGCTGGCGCGGCCCAAGCAGAGCCCTGACTAGGATGAC	2473
Qy	2573	AGCAGCAAAAGACCACTTTCTCCCTGAGAGAGCTTCTGCTACTCTGCTACCTGACCTGA	2632
Db	2474	AGCAGCAAAAGACCACTTTCTCCCTGAGAGAGCTTCTGCTACTCTGCTACCTGACCTGA	2533
Qy	2633	TGACACTCAGCAGGCTGATGCAAGCAGTCTGCTCCCTCCCTATGGGACTCCCTTTACCAA	2692
Db	2534	TGACACTCAGCAGGCTGATGCAAGCAGTCTGCTCCCTCCCTATGGGACTCCCTTTACCAA	2593
Qy	2693	GCATGTAGCTCTTAAACAGGCTGGGGGTACCCCGAGACCTGCTCTACCTGATATTG	2752
Db	2594	GCATGTAGCTCTTAAACAGGCTGGGGGTACCCCGAGACCTGCTCTACCTGATATTG	2653
Qy	2753	AAGAACTGGAGAGTCTTCAAGTCTGCGCATTTCCAGGAGCCCTCCAGAAACACAGTG	2812
Db	2654	AAGAACTGGAGAGTCTTCAAGTCTGCGCATTTCCAGGAGCCCTCCAGAAACACAGTG	2713
Qy	2813	TTTCAAGAGACCTTAAAAAACCCTGCTGTCAGAGACCTTATGTTGTAATGAAACCAACAA	2872
Db	2714	TTTCAAGAGACCTTAAAAAACCCTGCTGTCAGAGACCTTATGTTGTAATGAAACCAACAA	2773

PR	29-OCT-1998;	98US-0106248P.	DR	P-PSDB; ADC18146.	
PR	29-OCT-1998;	98US-0106384P.	XX	Novel isolated PRO polypeptides e.g. PRO1491 and PRO1571, useful in the	
PR	29-OCT-1998;	98US-0108500P.	PT	preparation of a medicament for treating a condition responsive to PRO	
PR	30-OCT-1998;	98US-0106464P.	PT	polypeptide, and as therapeutic agents e.g. vaccines.	
PR	03-NOV-1998;	98US-0106856P.	XX	Claim 2; SEQ ID NO 276; 555pp; English.	
PR	03-NOV-1998;	98US-0106802P.	XX	The invention relates to human PRO polypeptides and the polynucleotides	
PR	03-NOV-1998;	98US-0106905P.	XX	encoding them. The sequences are useful in the preparation of a	
PR	03-NOV-1998;	98US-0106919P.	CC	medicament for treating a condition responsive to a PRO polypeptide. The	
PR	03-NOV-1998;	98US-0106934P.	CC	polypeptides are useful in a number of functional biological assays, as	
PR	10-NOV-1998;	98US-0107783P.	CC	molecular weight markers for protein electrophoresis and as therapeutic	
PR	17-NOV-1998;	98US-0108775P.	CC		
PR	17-NOV-1998;	98US-0108779P.			
PR	17-NOV-1998;	98US-0108787P.			
PR	17-NOV-1998;	98US-0108788P.			
PR	17-NOV-1998;	98US-0108801P.			
PR	17-NOV-1998;	98US-0108802P.			
PR	17-NOV-1998;	98US-0108806P.			
PR	17-NOV-1998;	98US-0108807P.			
PR	17-NOV-1998;	98US-0108857P.			
PR	17-NOV-1998;	98US-0108925P.			
PR	18-NOV-1998;	98US-0108848P.			
PR	18-NOV-1998;	98US-0108849P.			
PR	18-NOV-1998;	98US-0108850P.			
PR	18-NOV-1998;	98US-0108851P.			
PR	18-NOV-1998;	98US-0108852P.			
PR	18-NOV-1998;	98US-0108858P.			
PR	18-NOV-1998;	98US-0108904P.			
PR	22-DEC-1998;	98US-0113296P.			
PR	30-DEC-1998;	98US-0114223P.			
PR	05-JAN-1999;	99WO-US000106.			
PR	16-JAN-1999;	99US-0129674P.			
PR	23-JUN-1999;	99US-0141037P.			
PR	20-JUL-1999;	99US-0144758P.			
PR	26-JUL-1999;	99US-0145698P.			
PR	01-SEP-1999;	99WO-US020111.			
PR	15-SEP-1999;	99WO-US021194.			
PR	29-OCT-1999;	99US-0162506P.			
PR	30-NOV-1999;	99WO-US028313.			
PR	02-DEC-1999;	99WO-US028551.			
PR	16-DEC-1999;	99WO-US030095.			
PR	05-JAN-2000;	2000WO-US000219.			
PR	06-JAN-2000;	2000WO-US000376.			
PR	11-FEB-2000;	2000WO-US003565.			
PR	18-FEB-2000;	2000WO-US004342.			
PR	24-FEB-2000;	2000WO-US005004.			
PR	02-MAR-2000;	2000WO-US005841.			
PR	15-MAR-2000;	2000WO-US006884.			
PR	17-MAY-2000;	2000WO-US013705.			
PR	22-MAY-2000;	2000WO-US014042.			
PR	30-MAY-2000;	2000WO-US014941.			
PR	02-JUN-2000;	2000WO-US015264.			
PR	23-AUG-2000;	2000WO-US023522.			
PR	24-AUG-2000;	2000WO-US023328.			
PR	08-NOV-2000;	2000WO-US030952.			
PR	10-NOV-2000;	2000WO-US030873.			
PR	01-DEC-2000;	2000WO-US032678.			
PR	28-FEB-2001;	2001WO-US006520.			
PR	01-MAR-2001;	2001WO-US006666.			
PR	01-JUN-2001;	2001WO-US017800.			
PR	20-JUN-2001;	2001WO-US019692.			
PR	29-JUN-2001;	2001WO-US021066.			
PR	09-JUL-2001;	2001WO-US021735.			
PR	04-SEP-2001;	2001US-00946374.			
XX	(GETH) GENENTECH INC.				
PA	Baker KP, Botstein D, Desnovers L, Eaton DL, Ferrara N, Fong S,				
XX	Gao W, Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ,				
PI	Pan J, Paoni NF, Roy MA, Smith V, Stewart TA, Tumas D, Watanabe CK;				
PI	Williams PW, Wood WI;				
XX	WPI; 2003-555602/52.				
DR					

QY 1013 GAAATGACGTGGCGCGGAAAGAGCTGCTGCAGAGAGAGTGGACCAACCTTCTCTGAAGGCCCA 1072
Db 914 GAAATGACGTGGCGCGCGGAAAGAGCTGCTGCAGAGAGAGTGGACCAACCTTCTCTGAAGGCCCA 973
QY 1073 GCTGCTCTGCACCCAGACCGCGGCGAGCTGCCCTTCAAGCTCATCGCGCACGCGGTCTCTGCT 1132
Db 974 GCTGCTCTGCACCCAGACCGCGGCGAGCTGCCCTTCAAGCTCATCGCGCACGCGGTCTCTGCT 1033
QY 1133 CCCCAGGATTTCTCCACAGCTCCCAACATCTACGAGTCTTCACTCTCCAGTGGAGGT 1192
Db 1034 CCCCAGGATTTCTCCACAGCTCCCAACATCTACGAGTCTTCACTCTCCAGTGGAGGT 1093
QY 1193 TGGCGGACCAAGAGCTCTCGGCTTTGCTCTCTCTCTGACATTTGAAGCTGCTCT 1252
Db 1094 TGGCGGACCAAGAGCTCTCGGCTTTGCTCTCTCTCTGACATTTGAAGCTGCTCT 1153
QY 1253 TAAGGGGAAATACAAAGATTGAACAAAGAAATTCACGCTGAGCTACTTATAGGGGCC 1312
Db 1154 TAAGGGGAAATACAAAGATTGAACAAAGAAATTCACGCTGAGCTACTTATAGGGGCC 1213
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Db 1274 CTTTATGAGGACCAATTTCTGATGATGAGTGAAGTGGGACGCGCTGCTGCTGAA 1333
QY 1433 ATCTGGCGTGAGTATACAGGCTTGCAAGTGGAGACAGCCAGGCTTGATGGGACAG 1492
Db 1334 ATCTGGCGTGAGTATACAGGCTTGCAAGTGGAGACAGCCAGGCTTGATGGGACAG 1393
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Db 1814 TGTCCCTTAATCTCTGAGCTCTCCCTGCCCCACCTGTGAGCTTGGCTCTTTATTA 1873
QY 1973 TTGGAGTCAATGGCCAGCAGCTGCCAGAGCTCTTCACTGTCTCAATAGGCTCCCT 2032
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QY 2033 CTTGCTGATGATGAGTGGAGTGGGCTTCTTACAGTGTGGGCACTGAGAAATGG 2092
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QY 2093 CTTTTCATACCTGTGATCTCTACTGGTGGACAGCCAGACCCCTGGCCCTGGA 2152
Db 1994 CTTTTCATACCTGTGATCTCTACTGGTGGACAGCCAGACCCCTGGCCCTGGA 2053
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QY 3053 TGCTTCAAGTGGGCGAGCTGATCCCTTCTGCTGCGGAGATGGCAGGCTTACTG 3112
Db 2954 TGCTTCAAGTGGGCGAGCTGATCCCTTCTGCTGCGGAGATGGCAGGCTTACTG 3013
QY 3113 AGCCTTCTTCACTCTTTTACCTAGTGTGACCCCTTCACTCTCCCTCTCCCTTTCTTCT 3172
Db 3014 AGCCTTCTTCACTCTTTTACCTAGTGTGACCCCTTCACTCTCCCTCTCCCTTTCTTCT 3073
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Qv	3233	CTTA 3236	
Db	3134	CTTA 3137	

RESULT 6
ADD70791
ID ADD70791 standard; cDNA; 3143 BP.
XX
AC ADD70791;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human cDNA encoding secreted/transmembrane protein PRO1317.
XX
KW Human; ss; gene; secreted protein; transmembrane protein; PRO; tumour;
KW immune response; cardiac insufficiency disorder; calcium flux;
KW umbilical vein endothelial cell; bone disorder; cartilage disorder;
KW arthritis; wound healing; diabetes; skeletal muscle cells; obesity;
KW Berger disease; nephropathy; Schonlein-Henoch purpura; coeliac disease;
KW dermatitis; herpeticiformis; Crohn's disease; thalassaemia.
XX
OS Homo sapiens.
XX
XX US2003099625-A1.
XX
XX 29-MAY-2003.
XX
XX 12-DEC-2001; 2001US-00015386.
XX
XX 01-SEP-1998; 98US-0098716P.
XX 01-SEP-1998; 98US-0098723P.
XX 01-SEP-1998; 98US-0098749P.
XX 01-SEP-1998; 98US-0098750P.
XX 02-SEP-1998; 98US-0098803P.
XX 02-SEP-1998; 98US-0098821P.
XX 02-SEP-1998; 98US-0098843P.
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XX 09-SEP-1998; 98US-0099602P.
XX 09-SEP-1998; 98US-0099642P.
XX 10-SEP-1998; 98US-0099741P.
XX 10-SEP-1998; 98US-0099754P.
XX 10-SEP-1998; 98US-0099792P.
XX 10-SEP-1998; 98US-0099808P.
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XX 10-SEP-1998; 98US-0099815P.
XX 10-SEP-1998; 98US-0099816P.
XX 15-SEP-1998; 98US-0100385P.
XX 15-SEP-1998; 98US-0100388P.
XX 15-SEP-1998; 98US-0100390P.
XX 16-SEP-1998; 98US-0100584P.
XX 16-SEP-1998; 98US-0100627P.
XX 16-SEP-1998; 98US-0100661P.
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XX 16-SEP-1998; 98US-0100664P.
XX 17-SEP-1998; 98US-0100683P.
XX 17-SEP-1998; 98US-0100684P.
XX 17-SEP-1998; 98US-0100710P.
XX 17-SEP-1998; 98US-0100711P.
XX 17-SEP-1998; 98US-0100913P.
XX 17-SEP-1998; 98US-0100930P.
XX 18-SEP-1998; 98US-0100848P.
XX 18-SEP-1998; 98US-0100849P.
XX 18-SEP-1998; 98US-0101014P.
XX 18-SEP-1998; 98US-0101068P.
XX 18-SEP-1998; 98US-0101071P.
XX 22-SEP-1998; 98US-0101279P.

PR	23-SEP-1998;	98US-0101471P.
PR	23-SEP-1998;	98US-0101472P.
PR	23-SEP-1998;	98US-0101474P.
PR	23-SEP-1998;	98US-0101475P.
PR	23-SEP-1998;	98US-0101476P.
PR	23-SEP-1998;	98US-0101477P.
PR	23-SEP-1998;	98US-0101479P.
PR	24-SEP-1998;	98US-0101738P.
PR	24-SEP-1998;	98US-0101741P.
PR	24-SEP-1998;	98US-0101743P.
PR	24-SEP-1998;	98US-0101915P.
PR	24-SEP-1998;	98US-0101916P.
PR	29-SEP-1998;	98US-0102207P.
PR	29-SEP-1998;	98US-0102240P.
PR	29-SEP-1998;	98US-0102307P.
PR	29-SEP-1998;	98US-0102330P.
PR	29-SEP-1998;	98US-0102331P.
PR	30-SEP-1998;	98US-0102484P.
PR	30-SEP-1998;	98US-0102487P.
PR	30-SEP-1998;	98US-0102570P.
PR	30-SEP-1998;	98US-0102571P.
PR	01-OCT-1998;	98US-0102684P.
PR	01-OCT-1998;	98US-0102687P.
PR	02-OCT-1998;	98US-0102965P.
PR	06-OCT-1998;	98US-0103258P.
PR	06-OCT-1998;	98US-0103449P.
PR	07-OCT-1998;	98US-0103314P.
PR	07-OCT-1998;	98US-0103315P.
PR	07-OCT-1998;	98US-0103328P.
PR	07-OCT-1998;	98US-0103355P.
PR	07-OCT-1998;	98US-0103396P.
PR	07-OCT-1998;	98US-0103401P.
PR	08-OCT-1998;	98US-0103633P.
PR	08-OCT-1998;	98US-0103678P.
PR	08-OCT-1998;	98US-0103679P.
PR	08-OCT-1998;	98US-0103711P.
PR	14-OCT-1998;	98US-0104257P.
PR	20-OCT-1998;	98US-0104987P.
PR	20-OCT-1998;	98US-0105000P.
PR	21-OCT-1998;	98US-0105002P.
PR	22-OCT-1998;	98US-0105104P.
PR	22-OCT-1998;	98US-0105169P.
PR	22-OCT-1998;	98US-0105266P.
PR	26-OCT-1998;	98US-0105693P.
PR	26-OCT-1998;	98US-0105694P.
PR	27-OCT-1998;	98US-0105807P.
PR	27-OCT-1998;	98US-0105881P.
PR	27-OCT-1998;	98US-0105882P.
PR	27-OCT-1998;	98US-0106062P.
PR	28-OCT-1998;	98US-0106023P.
PR	28-OCT-1998;	98US-0106029P.
PR	28-OCT-1998;	98US-0106030P.
PR	28-OCT-1998;	98US-0106032P.
PR	28-OCT-1998;	98US-0106033P.
PR	29-OCT-1998;	98US-0106178P.
PR	29-OCT-1998;	98US-0106248P.
PR	29-OCT-1998;	98US-0106384P.
PR	29-OCT-1998;	98US-0108500P.
PR	30-OCT-1998;	98US-0108464P.
PR	03-NOV-1998;	98US-0108565P.
PR	03-NOV-1998;	98US-0108566P.
PR	03-NOV-1998;	98US-0108905P.
PR	03-NOV-1998;	98US-0108919P.
PR	03-NOV-1998;	98US-0108932P.
PR	03-NOV-1998;	98US-0108934P.
PR	10-NOV-1998;	98US-0107782P.
PR	17-NOV-1998;	98US-0108775P.
PR	17-NOV-1998;	98US-0108779P.
PR	17-NOV-1998;	98US-0108787P.
PR	17-NOV-1998;	98US-0108788P.
PR	17-NOV-1998;	98US-0108801P.
PR	17-NOV-1998;	98US-0108802P.
PR	17-NOV-1998;	98US-0108806P.

Db 1214 TGAGACCAACCCCGGCCAGTGGTCTCAGTGGGCCCTCTCTGTATAAGGCCCTGTAC 1273
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Qy 1433 ATCTGGCGTGGAGTATACAGGCTTGCAAGTGGAGACAGCCAGCGCCCTTGATGGGCACAG 1492
Db 1334 ATCTGGCGTGGAGTATACAGGCTTGCAAGTGGAGACAGCCAGCGCCCTTGATGGGCACAG 1393
Qy 1493 CCATCTTGTGATGATCTGCTGAGTGGGAAACCAACAGGCTGCTCCACAGGCTGCTGTAAAGTG 1552
Db 1394 CCATCTTGTGATGATCTGCTGAGTGGGAAACCAACAGGCTGCTCCACAGGCTGCTGTAAAGTG 1453
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Db 1574 GAGGGTCCCCGAGCACTGCTAGTGTCTATGAGAGCTGTGTGACTGTGTCTTGGCCCG 1633
Qy 1733 GGACCCCCACCTGCTGGGACCCCTGAGTCCCGAACCTGTGCTCTGCTGCTGCCCCCAA 1792
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Qy 1793 CTTGAACTCTCGGAGAGCATGGAGCGGGGAAACCCAGAGTGGCAGTGGCCAGTGG 1852
Db 1694 CTTGAACTCTCGGAGAGCATGGAGCGGGGAAACCCAGAGTGGCAGTGGCCAGTGG 1753
Qy 1853 CCCCATGAGCAGGAGCTTCCGCTTCAGAGCGCCCGCAATCATTAAGAAGTCTCTGGC 1912
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Qy 1913 TGTCCCTAACTCCATCTGAGTCCCTGCTGCCCCCAGCTGTGAGCTTGGCCCTTTATTA 1972
Db 1814 TGTCCCTAACTCCATCTGAGTCCCTGCTGCCCCCAGCTGTGAGCTTGGCCCTTTATTA 1873
Qy 1973 TTGGAGTCATGGCCCGCAGCAGTCCCAAGAGCTCTTCCACTGTCTACAAATGGCTCCCT 2032
Db 1874 TTGGAGTCATGGCCCGCAGCAGTCCCAAGAGCTCTTCCACTGTCTACAAATGGCTCCCT 1933
Qy 2033 CTTGCTGATGAGCAGGATGAGTGGGGTCTCTACAGTGTCTGGGCAACTGAGATGG 2092
Db 1934 CTTGCTGATGAGCAGGATGAGTGGGGTCTCTACAGTGTCTGGGCAACTGAGATGG 1993
Qy 2093 CTTTTCATACCTGTGATCTCCTACTGCTGAGCAGCAGCAGACCCCTGGGCCCTGGA 2152
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Db 2294 AAGCAGAGAGCAACCTCCAGTCTCCCAAGAAATGACAGGACCTCTGCCAGTGTATGGA 2353
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Db 2354 CGCTGACAAACCTGCTAGGCACTGAGGTAGCTTAACTCTAGGCAAGCCCGGGCTG 2413
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Db 2534 TGACACTCAGCAGGCTGATGACAGCAGTCTGCTCCCTATGGACTCCCTTCTACCAA 2593
Qy 2693 GCACATGAGCTCTCTAAACAGGCTGGGGCTACCCCGACAGCTCTCTACACTGATATTG 2752
Db 2594 GCACATGAGCTCTCTAAACAGGCTGGGGCTACCCCGACAGCTCTCTACACTGATATTG 2653
Qy 2753 AAGAACTCTGAGAGGATCTTTCAGTCTGGGCATTTCCAGGACCCCTCCAGAAACACAGTG 2812
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Db 2834 GGACACCACTCTCTCTCTCCAGGCTCATGAGGATCTGCTCTCTCTCTCTCTCT 2893
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Db 2894 ACCAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2953
Qy 3053 TGTTCAGTGGGGAGACTCTGATCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3112
Db 2954 TGTTCAGTGGGGAGACTCTGATCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3013
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Db 3014 AGCTTCTTCTCCT 3073
Qy 3173 GTTTTGGGATTCAGAAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3232
Db 3074 GTTTTGGGATTCAGAAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3133
Qy 3233 CTTA 3236
Db 3134 CTTA 3137

RESULT 7

ADD39868
ID ADD39868 standard; cDNA; 3143 BP.

XX ADD39868;

DT 15-JAN-2004 (first entry)

XX Human cDNA encoding secreted/transmembrane protein PRO1317.

XX Human; ss; gene; secreted protein; transmembrane protein; PRO; tumour;
KW immune response; cardiac insufficiency disorder; calcium flux;
KW umbilical vein endothelial cell; bone disorder; cartilage disorder;
KW arthritis; wound healing; diabetes; skeletal muscle cells; obesity;

KW Berger disease; nephropathy; Schonlein-Henoch purpura; coeliac disease;
KW dermatitis; herpeticiformis; Crohn's disease; thalassaemia.
XX Homo sapiens.
XX US2003083462-A1.
XX 01-MAY-2003.
XX 10-DEC-2001; 2001US-00013913.
XX 05-JAN-1999; 99WO-US000106.
XX 01-SEP-1999; 99WO-US020111.
XX 15-SEP-1999; 99WO-US021194.
XX 30-NOV-1999; 99WO-US028313.
XX 02-DEC-1999; 99WO-US028551.
XX 16-DEC-1999; 99WO-US030095.
XX 05-JAN-2000; 2000WO-US000219.
XX 06-JAN-2000; 2000WO-US000376.
XX 11-FEB-2000; 2000WO-US003565.
XX 18-FEB-2000; 2000WO-US004342.
XX 24-FEB-2000; 2000WO-US005004.
XX 02-MAR-2000; 2000WO-US005841.
XX 15-MAR-2000; 2000WO-US006884.
XX 17-MAY-2000; 2000WO-US013705.
XX 22-MAY-2000; 2000WO-US014042.
XX 30-MAY-2000; 2000WO-US014941.
XX 02-JUN-2000; 2000WO-US015264.
XX 23-AUG-2000; 2000WO-US023522.
XX 24-AUG-2000; 2000WO-US023328.
XX 08-NOV-2000; 2000WO-US030952.
XX 10-NOV-2000; 2000WO-US030873.
XX 01-DEC-2000; 2000WO-US032878.
XX 28-FEB-2001; 2001WO-US006520.
XX 01-MAR-2001; 2001WO-US006666.
XX 01-JUN-2001; 2001WO-US017800.
XX 20-JUN-2001; 2001WO-US019692.
XX 29-JUN-2001; 2001WO-US021066.
XX 09-JUL-2001; 2001WO-US021735.
XX 04-SEP-2001; 2001US-00946374.
XX (GETH) GENENTECH INC.
XX Baker KP, Botstein D, Desnoyers L, Eaton DL, Ferrara N, Fong S;
XX Gao W, Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ;
XX Pan J, Paoni NF, Roy MA, Smith V, Stewart TA, Tumas D, Watanabe CK;
XX Williams PM, Wood WI;
XX WPI; 2003-755122/71.
XX P-PSDB; ADD39869.
XX New secreted and transmembrane PRO polypeptides useful for treating
XX cancers, kidney disorders, Crohn's disease, diabetes mellitus, hyper- or
XX hypo-insulinemia, sports injuries and arthritis.
XX Claim 2; SEQ ID NO 276; 557pp; English.
XX The invention relates to an isolated PRO polypeptide (secreted or
XX transmembrane protein) having at least 80% amino acid sequence identity
XX to an amino acid sequence chosen from 123 fully defined sequences as
XX given in the specification (including their extracellular domains either
XX or without their associated signal peptides. Also include are the
XX nucleotide (NA) sequences encoding PRO, a vector comprising the PRO NA, a
XX host cell comprising the vector, producing PRO, a chimeric molecule
XX comprising PRO fused to a heterologous amino acid sequence, and an anti-
XX PRO antibody. PRO is useful as molecular weight markers for protein
XX electrophoresis and also for chromosome identification. PRO is also
XX useful for tissue typing. PRO and PRO NA are useful as hybridisation
XX probes for a cDNA library to isolate the full-length PRO cDNA. PRO NA is
XX useful for generating transgenic animals or knock-out animals which are
XX useful for development and screening useful reagents. PRO NA is also
XX useful in gene therapy. PRO1244, PRO1286 and PRO1303 polypeptides are
XX useful for treating cancerous tumours. PRO1250, PRO1418 and PRO1410

CC polypeptides are useful for suppressing immune response. PRO1246
CC polypeptide is useful for treating cardiac insufficiency disorders.
CC PRO1246 polypeptide is also useful for treating tumours. PRO1246 and
CC PRO1561 polypeptide are useful for stimulating calcium flux in human
CC umbilical vein endothelial cells. PRO1265, PRO1250 and PRO1474
CC polypeptides are useful for treating bone and/or cartilage disorders
CC (e.g., arthritis) and wound healing. PRO1130, PRO1275 and PRO1418
CC polypeptides are useful for treating diabetes in skeletal muscle cells
CC and obesity. PRO1265, PRO1244 and PRO1382 polypeptides are useful for
CC treating Berger disease or other nephropathies associated with Schonlein-
CC Henoch purpura, coeliac disease, dermatitis, herpeticiformis or Crohn's
CC disease. PRO1478, PRO1465, PRO1412, PRO1279, PRO1304, PRO1306, PRO1418,
CC PRO1410 and PRO1575 are useful in treating thalassaemias. The present
XX sequence encodes a PRO protein of the invention.
XX
SQ Sequence 3143 BP; 656 A; 963 C; 828 G; 696 T; 0 U; 0 Other;

Query Match 87.3%; Score 3060.8; DB 9; Length 3143;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 3062; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 173 AGAGTCCCTGGTGACAGTCTGTGGCTGAGCATGGCCCTCCAGCCCTGGGCTGGACCC 232
DB |||||
74 AGAGTCCCTGGTGACAGTCTGTGGCTGAGCATGGCCCTCCAGCCCTGGGCTGGACCC 133
QY 233 CTGGAGCCTCTGGGCGCTTTCTCTCCAACTCTTCAGCTGCTGCCGAGAGACAC 292
DB |||||
134 CTGGAGCCTCTGGGCGCTTTCTCTCCAACTCTTCAGCTGCTGCCGAGAGACAC 193
QY 293 CGCGGGGGAGCGGGCGAGGGGCCCATGCCAGGCTCAGATATCTGACGGGGATGAACG 352
DB |||||
194 CGCGGGGGAGCGGGCGAGGGGCCCATGCCAGGCTCAGATATCTGACGGGGATGAACG 253
QY 353 TAGGGCACTTAGCTTCTTCCACGAGGGGCTCCAGATTTTGACACTCTGCTCCTGAG 412
DB |||||
254 TAGGGCACTTAGCTTCTTCCACGAGGGGCTCCAGATTTTGACACTCTGCTCCTGAG 313
QY 413 TGGTGATGGAATACTCTCTACGTGGGGCTCGAGAGCCATTTCTGGCTTTGGATATCCA 472
DB |||||
314 TGGTGATGGAATACTCTCTACGTGGGGCTCGAGAGCCATTTCTGGCTTTGGATATCCA 373
QY 473 GGATCAGGGGTCCCGGAGGCTTAAGAAATATGATACCTGGCCAGGCTGACAGAAAAA 532
DB |||||
374 GGATCAGGGGTCCCGGAGGCTTAAGAAATATGATACCTGGCCAGGCTGACAGAAAAA 433
QY 533 GAGTCAATGTGCTTTAAGAAAGAGAGCAATGAGACACAGTGTGTTCAACTTTCATCCGTGT 592
DB |||||
434 GAGTCAATGTGCTTTAAGAAAGAGAGCAATGAGACACAGTGTGTTCAACTTTCATCCGTGT 493
QY 593 CTGTGTTCTTACAATGTCACCATCTCTACCTGGGGACCTTCGGCTTCAGCCCTGC 652
DB |||||
494 CTGTGTTCTTACAATGTCACCATCTCTACCTGGGGACCTTCGGCTTCAGCCCTGC 553
QY 653 TTGTACCTTCATTGAACTTCAAGATTTCTACTGTGGCCATCTCGAGAGGCAAGGTGAT 712
DB |||||
554 TTGTACCTTCATTGAACTTCAAGATTTCTACTGTGGCCATCTCGAGAGGCAAGGTGAT 613
QY 713 GGAGGAAAAGCCAAAGCCCTTTGACCCGCTCAAGCATAGCGGTGTCTTGGTGGG 772
DB |||||
614 GGAGGAAAAGCCAAAGCCCTTTGACCCGCTCAAGCATAGCGGTGTCTTGGTGGG 673
QY 773 TGGGATGCTCTATTCTGTGTACTATGAACAATCTCTGGGCGAGTGGCCCATCTCATCGG 832
DB |||||
674 TGGGATGCTCTATTCTGTGTACTATGAACAATCTCTGGGCGAGTGGCCCATCTCATCGG 733
QY 833 CACACTGGGATCCAGCCTGTCTCTCAAGACCGACAACTTCTCCGCTGGGTGCATCATGA 892
DB |||||
734 CACACTGGGATCCAGCCTGTCTCTCAAGACCGACAACTTCTCCGCTGGGTGCATCATGA 793
QY 893 CGCCTCCTTTGGGAGGAGCATCCCTTCGACCCAGGTGCTACTTCTTCTTCGAGGAGAC 952
DB |||||
794 CGCCTCCTTTGGGAGGAGCATCCCTTCGACCCAGGTGCTACTTCTTCTTCTTCGAGGAGAC 853

QY 953 AGCCAGGAGTTTCTTCTTTGAGAGCTCCACATCGGGTGGCTAGAGTCTGCAG 1012
DB 854 AGCCAGGAGTTTCTTCTTTGAGAGCTCCACATCGGGTGGCTAGAGTCTGCAG 913
QY 1013 GAATGACGTGGCGGCGGAGAAAGCTGCTGCGAAGAGTGCACCACTTCTGTAAGGCCCA 1072
DB 914 GAATGACGTGGCGGCGGAGAAAGCTGCTGCGAAGAGTGCACCACTTCTGTAAGGCCCA 973
QY 1073 GCTGCTGACCCAGACCGGGGAGCTGCCCTTCAACGTCTATCGCCACGCGTCTGTCT 1132
DB 974 GCTGCTGACCCAGACCGGGGAGCTGCCCTTCAACGTCTATCGCCACGCGTCTGTCT 1033
QY 1133 CCGCGCGATCTTCCCAAGCTCCCAATCTACGAGTCTTCACTTCCAGTGCAGGT 1192
DB 1034 CCGCGCGATCTTCCCAAGCTCCCAATCTACGAGTCTTCACTTCCAGTGCAGGT 1093
QY 1193 TGGCGGACAGGAGCTCTGGGTTTGTGCTTCTCTCTTGGACATTAAGAGTCTT 1252
DB 1094 TGGCGGACAGGAGCTCTGGGTTTGTGCTTCTCTCTTGGACATTAAGAGTCTT 1153
QY 1253 TAAGGGGAAATACAAAGAGTTGAAACAAAGAAATTCACGCTGGAATCTTATAGGGGCC 1312
DB 1154 TAAGGGGAAATACAAAGAGTTGAAACAAAGAAATTCACGCTGGAATCTTATAGGGGCC 1213
QY 1313 TGAGACCAACCCCGGCGGAGCTTGTCTAGTGGGCGCTCTCTCTGATTAAGGCGCTGAC 1372
DB 1214 TGAGACCAACCCCGGCGGAGCTTGTCTAGTGGGCGCTCTCTCTGATTAAGGCGCTGAC 1273
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DB 1274 CTTTCAATGAAGACCAATTTCTGTATGAGTGAAGTGGTGGGAGCGCCCTGTGTGTAA 1333
QY 1433 ATCTGGGCTGAGATATACAGGCTTGCAGTGGAGACAGCCAGGCTTGAATGGGACAG 1492
DB 1334 ATCTGGGCTGAGATATACAGGCTTGCAGTGGAGACAGCCAGGCTTGAATGGGACAG 1393
QY 1493 CCATCTTGTCTATGTACCTGGGAAACACACAGGCTGCTCCACAGGCTGTGTGTGTGG 1552
DB 1394 CCATCTTGTCTATGTACCTGGGAAACACACAGGCTGCTCCACAGGCTGTGTGTGTGG 1453
QY 1553 GGAAGAGTCTCTATCTGTGTGAAGAGATTCAGCTGTTCCTGACCCCTGAACTGTGTG 1612
DB 1454 GGAAGAGTCTCTATCTGTGTGAAGAGATTCAGCTGTTCCTGACCCCTGAACTGTGTG 1513
QY 1613 CAACCTGAGCTGCCCCACCCAGGCTGCACTGTGTTGAGGCTTCTCAGAGTGTCTG 1672
DB 1514 CAACCTGAGCTGCCCCACCCAGGCTGCACTGTGTTGAGGCTTCTCAGAGTGTCTG 1573
QY 1673 GAGGTCGCCCGAGCCAACTGTAGTGTCTATGAGAGCTGTGTGACCTGTGTCTTGCCCG 1732
DB 1574 GAGGTCGCCCGAGCCAACTGTAGTGTCTATGAGAGCTGTGTGACCTGTGTCTTGCCCG 1633
QY 1733 GGACCCCACTGTGCTGGACCTGAGTCCCGAACCTGTGCTCTGCTGCTGCCCCAA 1792
DB 1634 GGACCCCACTGTGCTGGACCTGAGTCCCGAACCTGTGCTCTGCTGCTGCCCCAA 1693
QY 1793 CTTGAATCTCTGGAAGCAGGACATGGAGCGGGGAAACCCAGAGTGGCATGTGCCAGTGG 1852
DB 1694 CTTGAATCTCTGGAAGCAGGACATGGAGCGGGGAAACCCAGAGTGGCATGTGCCAGTGG 1753
QY 1853 CCCCATGAGCAGGAGCTTCCGCTCTAGAGCGCGCCGCAATCATTAAGAGTCTGCGC 1912
DB 1754 CCCCATGAGCAGGAGCTTCCGCTCTAGAGCGCGCCGCAATCATTAAGAGTCTGCGC 1813
QY 1913 TGTCTTAACTCTCTGAGCTCTCCCTGCGCCCACTGTGACCTTGGCCTCTTATTA 1972
DB 1814 TGTCTTAACTCTCTGAGCTCTCCCTGCGCCCACTGTGACCTTGGCCTCTTATTA 1873
QY 1973 TTGAGTCTATGGCCAGCAGGCTCTCCAGAGCTCTTCCACTGTCTACAAATGGCTCCCT 2032
DB 1874 TTGAGTCTATGGCCAGCAGGCTCTCCAGAGCTCTTCCACTGTCTACAAATGGCTCCCT 1933
QY 2033 CTTGCTGATAGTGACGAGTGGTGGGGTCTCTACCAAGTGTGGGCACTGAGAAATGG 2092

DB 1934 CTTGCTGATAGTGACGAGTGGAGTTGGGGTCTCTACCAAGTCTGGGCACTGAGAAATGG 1993
QY 2093 CTTTTCATACCTCTGTGATCTCTACTGGTGGAGAGCCAGGACAGACCTGGCCCTGGA 2152
DB 1994 CTTTTCATACCTCTGTGATCTCTACTGGTGGAGAGCCAGGACAGACCTGGCCCTGGA 2053
QY 2153 TCTCTGAATGGCAGGACATCCCCCGGAGCATGTGAAGGTCCCGTTGACACAGGTCAGTGG 2212
DB 2054 TCTCTGAATGGCAGGACATCCCCCGGAGCATGTGAAGGTCCCGTTGACACAGGTCAGTGG 2113
QY 2213 TGGGCGCGCTGGCTGGCCAGCAGTCTCTACTGGCCCGCCACTTGTCACTGTCACTGTCT 2272
DB 2114 TGGGCGCGCTGGCTGGCCAGCAGTCTCTACTGGCCCGCCACTTGTCACTGTCACTGTCT 2173
QY 2273 CTTTTCCTTAGTGTCTTTCAGGAGCCCTCATCATCTCTGTCGCTCCCTCCCAATGAGAGCACT 2332
DB 2174 CTTTTCCTTAGTGTCTTTCAGGAGCCCTCATCATCTCTGTCGCTCCCTCCCAATGAGAGCACT 2233
QY 2333 CCGGCTCGGGCAAGGTTTTCAGGCTGTGAGACCTCTGCGCTCTGGGAGAGAGCCCGTT 2392
DB 2234 CCGGCTCGGGCAAGGTTTTCAGGCTGTGAGACCTCTGCGCTCTGGGAGAGAGCCCGTT 2293
QY 2393 AAGCAGAGAGCAACACCTTCCAGTCTCCCAAGGAATGACAGGACCTCTGCGAGTGTGGA 2452
DB 2294 AAGCAGAGAGCAACACCTTCCAGTCTCCCAAGGAATGACAGGACCTCTGCGAGTGTGGA 2353
QY 2453 CGCTGAACAACTCTGCTAGGCACTGAGGTAGCTTAACTCTTAGGCAACAGGCGGGGCTG 2512
DB 2354 CGCTGAACAACTCTGCTAGGCACTGAGGTAGCTTAACTCTTAGGCAACAGGCGGGGCTG 2413
QY 2513 CCGTCAGGACCTTGCCCATCTGCTGGCGGCGGCAAGCAGCAGCCTGACTAGGATGAC 2572
DB 2414 CCGTCAGGACCTTGCCCATCTGCTGGCGGCGGCAAGCAGCAGCCTGACTAGGATGAC 2473
QY 2573 AGCAGCACAACAAAGACCACTTCTCTCTGAGAGAGCTTCTGTACTCTGTCATCACTGA 2632
DB 2474 AGCAGCACAACAAAGACCACTTCTCTCTGAGAGAGCTTCTGTACTCTGTCATCACTGA 2533
QY 2633 TGACACTCAGCAGGCTGATGACAGAGTCTGCTCTGCTCCCTATGGACCTCCCTTCTACCAA 2692
DB 2534 TGACACTCAGCAGGCTGATGACAGAGTCTGCTCTGCTCCCTATGGACCTCCCTTCTACCAA 2593
QY 2693 GCACATGAGCTCTTAAACAGGCTGGGGCTACCCCGCAGACCTGCTCTACACTGATATG 2752
DB 2594 GCACATGAGCTCTTAAACAGGCTGGGGCTACCCCGCAGACCTGCTCTACACTGATATG 2653
QY 2753 AAGAACCTGGAGAGATCTTTCAGTCTGGCCATTCAGGAGCCCTCCAGAAACACAGTG 2812
DB 2654 AAGAACCTGGAGAGATCTTTCAGTCTGGCCATTCAGGAGCCCTCCAGAAACACAGTG 2713
QY 2813 TTTTCAAGAGACCTTAAAAAACCCTGCTGTCCAGGACCTTATGGTAATGAACACCAAAACA 2872
DB 2714 TTTTCAAGAGACCTTAAAAAACCCTGCTGTCCAGGACCTTATGGTAATGAACACCAAAACA 2773
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DB 2774 TCTAAACATATATGCTTAAATGCACTCTCTGGAACCTCCACTCTGAAGCTGCGGCTTT 2833
QY 2933 GGACACCAACACTCTCTCTCCAGGCTCATGACAGGATCTGCTCCCTCTGCTTCCCTTT 2992
DB 2834 GGACACCAACACTCTCTCTCCAGGCTCATGACAGGATCTGCTCCCTCTGCTTCCCTTT 2893
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DB 2894 ACCAGTCTGCACTCTGCTCCAGGAGTCTTTCCTGAAGTCTGACCACTTCTTCTCT 2953
QY 3053 TGTCTCAGTTGGGCGAGCTCTGATCCCTCTGCGCTGCGAATGGCAGGAGTAACTG 3112
DB 2954 TGTCTCAGTTGGGCGAGCTCTGATCCCTCTGCGCTGCGAATGGCAGGAGTAACTG 3013
QY 3113 AGCCTTCTTCACTCTCTTACCTAGTGAACCTTCACTCTCCCTCTCCCTTTTCTTTT 3172

Db 1154 TAAGGGGAATACAAAGAGTTGAAACAAAGAACTTCCAGCTGGACTACTATTAGGGGGCC 1213
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 Db 1214 TGAGACCAACCCCGCCGAGGAGTTGCTCAGTGGGCCCTCTCTGTGATAAGCCCTGCAC 1273
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 Db 1334 ATCTGGCGTGGAGTATACACGGCTTCCAGTGGAGACAGCCACGGGCTTTGATGGGCACAG 1393
 QY 1493 CCACTCTGTCATGCTCTGGGAACCAACCAAGGTCGCTCCACAGGCTGTGGTAAAGTG 1552
 Db 1394 CCACTCTGTCATGCTCTGGGAACCAACCAAGGTCGCTCCACAGGCTGTGGTAAAGTG 1453
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XX ADD38435;
 AC ADD38435;
 XX 15-JAN-2004 (first entry)
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 KW Human; ss; gene; secreted protein; transmembrane protein; PRO; tumour;

immune response; cardiac insufficiency disorder; calcium flux;
umbilical vein endothelial cell; bone disorder; cartilage disorder;
arthritis; wound healing; diabetes; skeletal muscle cells; obesity;
Berger disease; nephropathy; Schönlein-Henoch purpura; coeliac disease;
dermatitis; herpeticiformis; Crohn's disease; thalassaemia.

Homo sapiens.

US2003096955-A1.

22-MAY-2003.

07-DEC-2001; 2001US-00012755.

01-SEP-1998; 98US-0098716P.
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05-JAN-1999; 99WO-US000106.
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RESULT 10
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ID ADD39391 standard; cDNA; 3143 BP.
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AC ADD39391;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human cDNA encoding secreted/transmembrane protein PRO1317.
XX
KW Human; ss; gene; secreted protein; transmembrane protein; PRO; tumour;
KW immune response; cardiac insufficiency disorder; calcium flux;
KW umbilical vein endothelial cell; bone disorder; cartilage disorder;
KW arthritis; wound healing; diabetes; skeletal muscle cells; obesity;
KW Berger disease; nephropathy; Schönlein-Henoch purpura; coeliac disease;
KW dermatitis; herpeticiformis; Crohn's disease; thalassemia.
XX
OS Homo sapiens.
XX
PN US2003096954-A1.
XX
PD 22-MAY-2003.
XX
PF 07-DEC-2001; 2001US-00011671.
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PR 17-NOV-1998; 98US-0108788P.
PR 17-NOV-1998; 98US-0108801P.
PR 17-NOV-1998; 98US-0108802P.
PR 17-NOV-1998; 98US-0108806P.
PR 17-NOV-1998; 98US-0108807P.
PR 17-NOV-1998; 98US-0108867P.
PR 17-NOV-1998; 98US-0108925P.
PR 18-NOV-1998; 98US-0108848P.
PR 18-NOV-1998; 98US-0108849P.
PR 18-NOV-1998; 98US-0108850P.
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PR 18-NOV-1998; 98US-0108852P.
PR 18-NOV-1998; 98US-0108858P.
PR 22-DEC-1998; 98US-0113296P.
PR 30-DEC-1998; 98US-0114223P.
PR 05-JAN-1999; 99WO-US000106.
PR 16-APR-1999; 99US-0129674P.
PR 23-JUN-1999; 99US-0141037P.
PR 20-JUL-1999; 99US-0144758P.
PR 26-JUL-1999; 99US-0145698P.
PR 01-SEP-1999; 99WO-US020111.
PR 15-SEP-1999; 99WO-US021194.
PR 29-OCT-1999; 99US-0162506P.
PR 30-NOV-1999; 99WO-US028313.
PR 02-DEC-1999; 99WO-US028551.
PR 16-DEC-1999; 99WO-US030095.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004342.
PR 24-FEB-2000; 2000WO-US005004.
PR 02-MAR-2000; 2000WO-US005841.
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PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 08-NOV-2000; 2000WO-US030952.
PR 10-NOV-2000; 2000WO-US030873.
PR 01-DEC-2000; 2000WO-US032678.
PR 28-FEB-2001; 2001WO-US006520.
PR 01-MAR-2001; 2001WO-US006666.

PR 01-JUN-2001; 2001WO-US017800.
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PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 04-SEP-2001; 2001US-00946374.
XX
FA (GETH) GENENTECH INC.
XX
PI Baker KP, Botstein D, Desnoyers L, Eaton DL, Ferrara N, Fong S,
PI Gao W, Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ,
PI Pan J, Paoni NF, Roy MA, Smith V, Stewart TA, Tumas D, Watanabe CK,
PI Williams PM, Wood WJ;
XX WPI; 2003-786999/74.
DR P-PSDB; ADD39392.
XX
XX
PT Novel isolated PRO polypeptide useful for tissue typing, modulating
PT biological activity of cell, as molecular weight markers in protein
PT electrophoresis, for treating arthritis, tumor.
XX
PS Claim 2; SEQ ID NO 276; 550pp; English.
CC The invention relates to an isolated PRO polypeptide (secreted or
Query Match 87.3%; Score 3060.8; DB 9; Length 3143;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 3062; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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XX
AC ADD38914;
XX
DT 15-JAN-2004 (first entry)
XX
Human cDNA encoding secreted/transmembrane protein PRO1317.
XX
DE Human; ss; gene; secreted protein; transmembrane protein; PRO; tumour;
KW immune response; cardiac insufficiency disorder; calcium flux;
KW umbilical vein endothelial cell; bone disorder; cartilage disorder;
KW arthritis; wound healing; diabetes; skeletal muscle cells; obesity;
KW Berger disease; nephropathy; Schönlain-Henoch purpura; coeliac disease;
KW dermatitis; herpeticiformis; Crohn's disease; thalassaemia.
XX
OS Homo sapiens.
XX
PN US2003092061-A1.
XX
PD 15-MAY-2003.
XX
PF 06-DEC-2001; 2001US-00007194.
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PR 01-SEP-1998; 98US-0098716P.
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PR 18-NOV-1998; 98US-0108858P.
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PR 22-DEC-1998; 98US-0113296P.
PR 30-DEC-1998; 98US-0114223P.
PR 05-JAN-1999; 99WO-US000106.
PR 16-JAN-1999; 99US-0129674P.
PR 23-JUN-1999; 99US-0141037P.
PR 20-JUL-1999; 99US-0144758P.
PR 28-JUL-1999; 99US-0145698P.
PR 01-SEP-1999; 99WO-US020111.
PR 15-SEP-1999; 99WO-US021194.
PR 29-OCT-1999; 99US-0162506P.
PR 30-NOV-1999; 99WO-US028313.
PR 02-DEC-1999; 99WO-US028551.
PR 16-DEC-1999; 99WO-US030095.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004342.
PR 24-FEB-2000; 2000WO-US005004.
PR 02-MAR-2000; 2000WO-US005841.
PR 15-MAR-2000; 2000WO-US006884.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 23-AUG-2000; 2000WO-US023522.
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PR 28-FEB-2001; 2001WO-US006520.
PR 01-MAR-2001; 2001WO-US006566.
PR 01-JUN-2001; 2001WO-US017800.
PR 20-JUN-2001; 2001WO-US019692.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 04-SEP-2001; 2001US-00946374.
XX (GETH) GENENTECH INC.
XX Baker KP, Botstein D, Desnoyers L, Eaton DL, Ferrara N, Fong S;
PI Bak W, Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ;
PI Pan J, Raoni NF, Roy MA, Smith V, Stewart TA, Tumas D, Watanabe CK;
PI Williams PM, Wood WI;
XX WPI; 2003-765477/72.
DR P-PSDB; ADD38915.
XX New isolated PRO polypeptide such as PRO1560, PRO444, PRO1018, PRO1773,
PT PRO1244, PRO1246, useful for treating cancerous tumors, cardiac
PT insufficiency disorders, wound healing, Crohn's disease, celiac disease.
XX Claim 2; SEQ ID NO 276; 555pp; English.
XX

CC The invention relates to an isolated PRO polypeptide (secreted or
Query Match 87.3%; Score 3060.8; DB 9; Length 3143;
Best local Similarity 99.9%; Pred. No. 0;
Matches 3062; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 173 AGAGTCCCTGGTGACAGTCTGTGGCTGAGCATGGCCCTCCAGCCCTGGCCCTGGACCC 232
DB 74 AGAGTCCCTGGTGACAGTCTGTGGCTGAGCATGGCCCTCCAGCCCTGGCCCTGGACCC 133

QY 233 CTGGAGCCTCTGGGCCCTTTTCTCTTCAACTGCTTCAGCTGCTGCTGCGACGACGAC 292
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QY 293 CGCGGGGGAGGGGGGAGGGGGCCATGCCAGGGTCAGATATATGACGGGATGAAG 352
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DB 374 GGATCCAGGGGTCCCAAGGCTTAAGAAATGATATACCGTGGCCAGCCAGTACAGAAATA 433

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DB 434 GAGTGAATGTCCCTTTAAGAGAGAGCAATGACACAGTGTTCAACTTCACTCCGTGT 493

QY 593 CCTGGTTTCTTACAAATGTCACCAATCTTACACCTGGGCACTTTCGCTTCAGCCCTGC 652
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QY 653 TTGTACCTTTCAATTTGAATCTCAAGATTCCTACTGTTCCTCATCTCGAGAGCAAGTCT 712
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DB 614 GGAGGAAAAGGCCAAAGCCCTTTGACCCCGCTCAAGCATACAGCTGTCTTGTGTGA 673

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QY 1073 GCTGCTCTGACCCAGCCGGGAGCTGCTTCTTCAAGCTCATTCGCGCCAGCGGCTCTGCT 1132
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QY 1373 CTTTATGAAGAACCATTTTCTGTATGAGCAAGTGGTGGGACGCCCTCTGCTGTGTGAA 1432
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QY 1433 ATCTGGCGTGGAGTATACACGGCTTGCAGTGGACACAGCCAGGGCTTCTGATGGGCACAG 1492
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QY 1493 CCATCTTGTCTATGTACCTGGGAAACACACAGGTCGCTCCACAAAGGCTGTGTAAAGTG 1552
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Db	2894	ACCAAGTCGTGACCGCT	GTGATCCCAAGGAAGTCTT	CCCTGAAAGCTGACCACTTCTTCT	2953
QY	3053	TGCTTCAGTTGGGGCAG	ACTCTGATCCCTTCTGCCC	TGGCAGAAATGCAGGGGTAATCTG	3112
Db	2954	TGCTTCAGTTGGGGCAG	ACTCTGATCCCTTCTGCCC	TGGCAGAAATGCAGGGGTAATCTG	3013
QY	3113	AGCCTTCTTCACTCCTT	TACCCCTAGCTGACCCCTT	CACTCTCCCTTCCCTTCCCTT	3172
Db	3014	AGCCTTCTTCACTCCTT	TACCCCTAGCTGACCCCTT	CACTCTCCCTTCCCTTCCCTT	3073
QY	3173	GTTTTGGGATTCAGAAA	AACTGCTTGTCTCAGAGAC	TGTTTTTTTTTATTAATAATAAGG	3232
Db	3074	GTTTTGGGATTCAGAAA	AACTGCTTGTCTCAGAGAC	TGTTTTTTTTTATTAATAATAAGG	3133
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Db	3134	CTTA	3137		

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ADD40345
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XX (GETH ) GENENTECH INC.
XX Baker KP, Botstein D, Desnoyers L, Eaton DL, Ferrara N, Fong S;
PI Gao W, Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ;
PI Pan J, Paoni NF, Roy MA, Smith V, Stewart TA, Tumas D, Watanabe CK;
PI Williams PM, Wood WI;
XX WPI; 2003-755104/71.
DR P-PSDB; ADD40346.
XX
XX New isolated PRO polypeptides such as PRO1560, PRO444, PRO1018, PRO1773,
PT PRO1244, PRO1246, are useful for treating cancerous tumors and cardiac
PT insufficiency disorders.
XX Claim 2; SEQ ID NO 276; 550pp; English.
XX The invention relates to an isolated PRO polypeptide (secreted or
CC Query Match 87.3%; Score 3060.8; DB 9; Length 3143;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 3062; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Db	2474	AGCAGCAGCAAAAGACACACCTTTCTCCCTGAGAGGAGCTTCTGCTACTCTGCATCACTGA	2533	PR	01-SEP-1998;	98US-0098723P.
QY	2633	TGACACTCAGCAGGGTGATGCACAGCAGTCTGCTCCCTATGGGACTCCCTTCTACCAA	2692	PR	01-SEP-1998;	98US-0098749P.
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QY	2693	GCACATGAGTCTCTTAACAGGGTGGGGGTACCCCCAGACCTGCTCTACACTGATATTG	2752	PR	02-SEP-1998;	98US-0098821P.
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Db	2834	GGACACCAACACTCCCTTCTCCAGGGTCATGCAAGGATCTGCTCCCTCTCTCCCTT	2893	PR	10-SEP-1998;	98US-0099932P.
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Db	2954	TGCTTCAGTTGGGGAGACTCTGATCCCTTCTGCTGAGGATCTGCTCCCTCTCTCTCT	3013	PR	10-SEP-1998;	98US-0099816P.
QY	3113	AGCTTCTTCACTCCCTTACCTTAGCTGACCTCCCTGAGTCTTCCCTGAGTCTGACCACTTCTCT	3172	PR	15-SEP-1998;	98US-0100385P.
Db	3014	AGCTTCTTCACTCCCTTACCTTAGCTGACCTCCCTGAGTCTTCCCTGAGTCTGACCACTTCTCT	3073	PR	15-SEP-1998;	98US-0100388P.
QY	3173	GTTTGGGATTCAGAAACTGCTTGTGACAGACTGTTATTTTATTTAAATATAAGG	3232	PR	15-SEP-1998;	98US-0100662P.
Db	3074	GTTTGGGATTCAGAAACTGCTTGTGACAGACTGTTATTTTATTTAAATATAAGG	3133	PR	15-SEP-1998;	98US-0100664P.
QY	3233	CTTA 3236		PR	16-SEP-1998;	98US-0100666P.
Db	3134	CTTA 3137		PR	16-SEP-1998;	98US-0100683P.
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ID	ADE50566 standard; cdna; 3143 BP.			PR	17-SEP-1998;	98US-0100919P.
AC	ADE50566;			PR	17-SEP-1998;	98US-0100930P.
DT	29-JAN-2004 (first entry)			PR	18-SEP-1998;	98US-0100848P.
XX	Human cdna encoding secreted/transmembrane protein PRO1317.			PR	18-SEP-1998;	98US-0100849P.
XX	Human; ss; gene; secreted protein; transmembrane protein; PRO; tumour;			PR	18-SEP-1998;	98US-0101014P.
XX	immune response; cardiac insufficiency disorder; calcium flux;			PR	18-SEP-1998;	98US-0101068P.
XX	umbilical vein endothelial cell; bone disorder; cartilage disorder;			PR	22-SEP-1998;	98US-0101279P.
XX	arthritis; wound healing; diabetes; skeletal muscle cells; obesity;			PR	23-SEP-1998;	98US-0101471P.
XX	Berger disease; nephropathy; Schonlein-Henoch purpura; coeliac disease;			PR	23-SEP-1998;	98US-0101472P.
XX	dermatitis; herpeticiformis; Crohn's disease; thalassemia.			PR	23-SEP-1998;	98US-0101474P.
OS	Homo sapiens.			PR	23-SEP-1998;	98US-0101475P.
XX	US2003069179-A1.			PR	23-SEP-1998;	98US-0101476P.
XX	10-APR-2003.			PR	23-SEP-1998;	98US-0101477P.
XX	11-DEC-2001; 2001US-00015393.			PR	23-SEP-1998;	98US-0101479P.
XX	01-SEP-1998; 98US-0098716P.			PR	24-SEP-1998;	98US-0101738P.
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				PR	29-SEP-1998;	98US-0102307P.
				PR	29-SEP-1998;	98US-0102330P.
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				PR	02-OCT-1998;	98US-0102965P.
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				PR	06-OCT-1998;	98US-0103449P.
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				PR	07-OCT-1998;	98US-0103315P.
				PR	07-OCT-1998;	98US-0103328P.
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				PR	07-OCT-1998;	98US-0103396P.
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RESULT 14
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DT 29-JAN-2004 (first entry)
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KW Human; ss; gene; secreted protein; transmembrane protein; PRO; tumour;
KW immune response; cardiac insufficiency disorder; calcium flux;
KW umbilical vein endothelial cell; bone disorder; cartilage disorder;
KW arthritis; wound healing; diabetes; skeletal muscle cells; obesity;
KW Berger disease; nephropathy; Schonlein-Henoch purpura; coeliac disease;
KW dermatitis; herpeticiformis; Crohn's disease; thalassaemia.
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XX
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XX
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PR 29-OCT-1998; 98US-0106248P.
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PR	29-OCT-1998;	98US-0106384P.	XX	New isolated PRO polypeptide useful for tissue typing, modulating
PR	29-OCT-1998;	98US-0108500P.	PT	biological activity of cell, as molecular weight markers in protein
PR	30-OCT-1998;	98US-0106464P.	PT	electrophoresis, for treating arthritis and tumors.
PR	03-NOV-1998;	98US-0106856P.	XX	Claim 2; SEQ ID NO 276; 555pp; English.
PR	03-NOV-1998;	98US-0106902P.	PS	The invention relates to an isolated PRO polypeptide (secreted or
PR	03-NOV-1998;	98US-0106905P.	CC	Query Match 87.3%; Score 3060.8; DB 9; Length 3143;
PR	03-NOV-1998;	98US-0106919P.		Best Local Similarity 99.9%; Pred. No. 0;
PR	03-NOV-1998;	98US-0106932P.		Matches 3062; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
PR	10-NOV-1998;	98US-0106934P.		
PR	10-NOV-1998;	98US-0107783P.	QY	173 AGAGTCCTCGGTGACAGTCTGTGGCTGAGATGGCCCTCCAGCCCTGGGCTGACACC 232
PR	17-NOV-1998;	98US-0108775P.	DB	74 AGAGTCCTCGGTGACAGTCTGTGGCTGAGATGGCCCTCCAGCCCTGGGCTGACACC 133
PR	17-NOV-1998;	98US-0108787P.	QY	233 CTGGAGCCTCTCGGCGCTTTTCTTCTTCCAACTGCTTCACTGCTGCTGCTGCGAGCAGC 292
PR	17-NOV-1998;	98US-0108801P.	DB	134 CTGGAGCCTCTCGGCGCTTTTCTTCTTCCAACTGCTTCACTGCTGCTGCTGCGAGCAGC 193
PR	17-NOV-1998;	98US-0108802P.	QY	293 CGCGGGGGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 352
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PR	17-NOV-1998;	98US-0108807P.	QY	353 TAGGGCACTTAGCTTCTTCCACAGAGGGCTCCAGAGTTTGGACACTGCTCTCTCTGAG 412
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PR	18-NOV-1998;	98US-0108848P.	QY	413 TGCTGATGGAATACTCTCTACGTGGGGCTCGAGAGCCATCTGGGCTTGGATATCCA 472
PR	18-NOV-1998;	98US-0108849P.	DB	314 TGCTGATGGAATACTCTCTACGTGGGGCTCGAGAGCCATCTGGGCTTGGATATCCA 373
PR	18-NOV-1998;	98US-0108850P.	QY	473 GGATCCAGGGTCCCGAGGCTTAAAGAACATGATACCTGGCCAGCCAGTGAAGAAAAA 532
PR	18-NOV-1998;	98US-0108851P.	DB	374 GGATCCAGGGTCCCGAGGCTTAAAGAACATGATACCTGGCCAGCCAGTGAAGAAAAA 433
PR	18-NOV-1998;	98US-0114223P.	QY	533 GAGTGAATGTGCTTTTAAAGAGAGAGCAATGAGACACAGTGTTCCTCACTTCCTCGTGT 592
PR	05-JAN-1999;	98US-0108904P.	DB	434 GAGTGAATGTGCTTTTAAAGAGAGAGCAATGAGACACAGTGTTCCTCACTTCCTCGTGT 493
PR	16-APR-1999;	98US-0129674P.	QY	593 CTGCTTTCTTACATGTCACCCATCTCTACCTGGGCGGCACTTCGCTTCAGCCCTGC 652
PR	23-JUN-1999;	99US-0141037P.	DB	494 CTGCTTTCTTACATGTCACCCATCTCTACCTGGGCGGCACTTCGCTTCAGCCCTGC 553
PR	26-JUL-1999;	99US-0144758P.	QY	653 TTGTACCTTCTTAACTGAACTTCAAGATTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTG 712
PR	01-SEP-1999;	99US-0145698P.	DB	554 TTGTACCTTCTTAACTGAACTTCAAGATTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTG 613
PR	15-SEP-1999;	99US-0162506P.	QY	713 GGAGGAAAAGGCCAAAGCCCTTTTGACCCCGCTTCAAGCATACGGCTGTCTTGGTGA 772
PR	29-OCT-1999;	99US-0162506P.	DB	614 GGAGGAAAAGGCCAAAGCCCTTTTGACCCCGCTTCAAGCATACGGCTGTCTTGGTGA 673
PR	30-NOV-1999;	99US-0162506P.	QY	773 TGGGATGCTTATTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 832
PR	02-DEC-1999;	99US-0162506P.	DB	674 TGGGATGCTTATTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 733
PR	05-JAN-2000;	2000WO-US000219.	QY	833 CACACTGGGATCCAGCCTGCTCTCAAGACCGCAACTTCCTCCGCTGGTGCATCATGA 892
PR	11-FEB-2000;	2000WO-US000376.	DB	734 CACACTGGGATCCAGCCTGCTCTCAAGACCGCAACTTCCTCCGCTGGTGCATCATGA 793
PR	18-FEB-2000;	2000WO-US004342.	QY	893 CGCCTTCTTTTGGGAGGCTGCTTCCAGCCAGGCTGCTTCTTCTTCTTCTTCTTCTTCTT 952
PR	24-FEB-2000;	2000WO-US005004.	DB	794 CGCCTTCTTTTGGGAGGCTGCTTCCAGCCAGGCTGCTTCTTCTTCTTCTTCTTCTTCTT 853
PR	02-MAR-2000;	2000WO-US005841.	QY	953 AGCCAGCAGGTTGACTTTCTTTTGAGAGGCTCCACACATTCGCGGGTGGCTAGAGTCTGCA 1012
PR	15-MAR-2000;	2000WO-US006884.	DB	854 AGCCAGCAGGTTGACTTTCTTTTGAGAGGCTCCACACATTCGCGGGTGGCTAGAGTCTGCA 913
PR	17-MAY-2000;	2000WO-US013705.	QY	1013 GAATGAGTGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1072
PR	30-MAY-2000;	2000WO-US014941.	DB	914 GAATGAGTGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 973
PR	02-JUN-2000;	2000WO-US015264.		
PR	23-AUG-2000;	2000WO-US023522.		
PR	08-NOV-2000;	2000WO-US030952.		
PR	10-NOV-2000;	2000WO-US030873.		
PR	01-DEC-2000;	2000WO-US032678.		
PR	28-FEB-2001;	2001WO-US006520.		
PR	01-MAR-2001;	2001WO-US006666.		
PR	20-JUN-2001;	2001WO-US017800.		
PR	29-JUN-2001;	2001WO-US019892.		
PR	09-JUL-2001;	2001WO-US021066.		
PR	04-SEP-2001;	2001WO-US021735.		
XX				
PA	(GETH) GENENTECH INC.			
XX				
PI	Baker KP, Botstein D, Deenoyers L, Eaton DL, Ferrara N, Fong S;			
PI	Gao W, Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ;			
PI	Pan J, Paoni NF, Roy MA, Smith V, Stewart TA, Tumas D, Watanabe			
PI	Williams PW, Wood WI;			
XX	WPI; 2003-765493/72.			
DR	P-PSDB; ADE20179.			

1073 GCTGCTCTGACCCAGCGGGCAGCTGCCCTTCAACGTCATCCGCCACGCGGTCTCTGCT 1132 QY
974 GCTGCTCTGACCCAGCGGGCAGCTGCCCTTCAACGTCATCCGCCACGCGGTCTCTGCT 1033 Db
1133 CCCGCCGATTTCTCCACAGCTCCCAACATACACAGCTCTTCACTCCCAAGTGGCAGGT 1192 QY
1034 CCCGCCGATTTCTCCACAGCTCCCAACATACACAGCTCTTCACTCCCAAGTGGCAGGT 1093 Db
1193 TGGCGGGACAGGAGCTCTGCGGTTTGTGCGTTCTCTCTTTGGACATTTGAACGTTGCTT 1252 QY
1094 TGGCGGGACAGGAGCTCTGCGGTTTGTGCGTTCTCTCTTTGGACATTTGAACGTTGCTT 1153 Db
1253 TTAGGGGAATACAAAGAGTTGAACAAAGAACTTCAAGTGGATCTTATAGGGGCC 1312 QY
1154 TTAGGGGAATACAAAGAGTTGAACAAAGAACTTCAAGTGGATCTTATAGGGGCC 1213 Db
1313 TGAGACCAACCCCGGCCAGGAGGTGCTCACTGGGCCCCCTCTCTGATAGAGCCCTGAC 1372 QY
1214 TGAGACCAACCCCGGCCAGGAGGTGCTCACTGGGCCCCCTCTCTGATAGAGCCCTGAC 1273 Db
1373 CTTTATGAAGAGCATTTCTCTGATGATGAGCAAGTGTGGGAGCGCCCTGCTGGTAA 1432 QY
1274 CTTTATGAAGAGCATTTCTCTGATGATGAGCAAGTGTGGGAGCGCCCTGCTGGTAA 1333 Db
1433 ATCTGCGTGGAGTATACACGGCTTGCAGTGGAGACGCCAGGGCTTTGATGGGCACAG 1492 QY
1334 ATCTGCGTGGAGTATACACGGCTTGCAGTGGAGACGCCAGGGCTTTGATGGGCACAG 1393 Db
1493 CCATCTTGTCTATGTAAGTGGGAAACACACAGGCTGCTTCAAGAGCTGTGGTAAAGTGG 1552 QY
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1613 CAACTTGTAGTGGGCCCCACACAGGCTGCAAGTGTGTAGGCTTCTCAGGAGTGTCTG 1672 QY
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1733 GGACCCCACTGTGCTGGGACCTCAGTCCGAACTGTTGCTCTGTCGCCCCCAA 1792 QY
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1913 TGTCCCTAATCATCTGAGAGTCTCCCTGCCGCCACCTGTACGCTTGGCTCTTATTA 1972 QY
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1874 TTGGAGTCAATGGCCAGCAGCAGTCCAGAAAGCTCTTCCAGTGTCTAATAGGCTCCCT 1933 Db
2033 CTTTGTGATGAGGATGGAGTGGGGTCTTACCAAGTGTGGGCAACTGAGAAAG 2092 QY
1934 CTTTGTGATGAGGATGGAGTGGGGTCTTACCAAGTGTGGGCAACTGAGAAAG 1993 Db
2093 CTTTTCATCCCTGTGATCTCTACTGGGTGGACAGCAGGACAGCCCTGGCCCTGGA 2152 QY
1994 CTTTTCATCCCTGTGATCTCTACTGGGTGGACAGCAGGACAGCCCTGGCCCTGGA 2053 Db
2153 TCCTGAACCTGGCAGGACATCCCCCGGGAGCATGTGAAGGTCCCCCTTGACCGAGGTGAGTGG 2212 QY

2054 TCCTGAACCTGGCAGGATCCCCCGGAGCATGTGAAGGTCCCGTTGACCAAGGTGAGTGG 2113 Db
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2333 CCGGGCTCGGGGCAAGGTTTCAGGGCTGTGAGACCTTCGCGCCCTGGGGGAGAGGCCCGCTT 2392 QY
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2453 CGCTGACCAACCTTCAGTCTAGGCACTGAGGTAGCTTAACTCTTAGGCACAGCCCGGGCTG 2512 QY
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2753 AAGAACTGAGAGGAGTCTCTAGTCTGGCCATTCAGGGACCTTCAGAAAACACAGT 2812 QY
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2873 TCTAAACAACTATGCTAAACATGCCACTCTCGAAAACCTCCACTCTGAAAGCTGCGGCTT 2932 QY
2774 TCTAAACAACTATGCTAAACATGCCACTCTCGAAAACCTCCACTCTGAAAGCTGCGGCTT 2833 Db
2933 GGACACCAACCTCTCTCCAGGGTCTGAGAGGATCTGCTCCCTGCTGCTTCCCTT 2992 QY
2834 GGACACCAACCTCTCTCCAGGGTCTGAGAGGATCTGCTCCCTGCTGCTTCCCTT 2893 Db
2993 ACCAGTCTGTCACCGCTGACTCCCGAGGAGTCTTCCCTGAAAGTCTGACCACTTCTTCT 3052 QY
2894 ACCAGTCTGTCACCGCTGACTCCCGAGGAGTCTTCTCTGAAAGTCTGACCACTTCTTCT 2953 Db
3053 TGTCTTCAAGTGGGGCAGACTCTGATTCCTTCTGCTGGCAGAGATGSCAGGGTAACTG 3112 QY
2954 TGTCTTCAAGTGGGGCAGACTCTGATTCCTTCTGCTGGCAGAGATGSCAGGGTAACTG 3013 Db
3113 AGCCTTCTCACTCTCTTTCAGCTGACCCCTTACCTCTCCCTGCTGCTTCTTCTTCT 3172 QY
3014 AGCCTTCTCACTCTCTTTCAGCTGACCCCTTACCTCTCCCTGCTGCTTCTTCTTCT 3073 Db
3173 GTTTTGGATTCAGAAAACCTGCTGTGAGAGCTGTTTATTTTATTAATAAATAAAGG 3232 QY
3074 GTTTTGGATTCAGAAAACCTGCTGTGAGAGCTGTTTATTTTATTAATAAATAAAGG 3133 Db
3233 CTTA 3236 QY

Db 3134 CTTA 3137

RESULT 15

ADE50089

ID ADE50089 standard; cDNA; 3143 BP.

XX AC ADE50089;

XX DT 29-JAN-2004 (first entry)

XX DE Human cDNA encoding secreted/transmembrane protein PRO1317.

XX KW Human; ss; gene; secreted protein; transmembrane protein; PRO; tumour;

XX KW immune response; cardiac insufficiency disorder; calcium flux;

XX KW umbilical vein endothelial cell; bone disorder; cartilage disorder;

XX KW arthritis; wound healing; diabetes; skeletal muscle cells; obesity;

XX KW Berger disease; nephropathy; Schönlein-Henoch purpura; coeliac disease;

XX KW dermatitis; herpeticiformis; Crohn's disease; thalassemia.

XX OS Homo sapiens.

XX FN US2003082626-A1.

XX PD 01-MAY-2003.

XX PF 06-DEC-2001; 2001US-00006116.

XX PR 01-SEP-1998; 98US-0098716P.

PR 01-SEP-1998; 98US-0098723P.

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PR 01-SEP-1998; 98US-0098750P.

PR 02-SEP-1998; 98US-0098803P.

PR 02-SEP-1998; 98US-0098821P.

PR 02-SEP-1998; 98US-0098843P.

PR 09-SEP-1998; 98US-0099536P.

PR 09-SEP-1998; 98US-0099596P.

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PR 10-SEP-1998; 98US-0099754P.

PR 10-SEP-1998; 98US-0099763P.

PR 10-SEP-1998; 98US-0099792P.

PR 10-SEP-1998; 98US-0099808P.

PR 10-SEP-1998; 98US-0099812P.

PR 10-SEP-1998; 98US-0099815P.

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PR 15-SEP-1998; 98US-0100388P.

PR 16-SEP-1998; 98US-0100390P.

PR 16-SEP-1998; 98US-0100584P.

PR 16-SEP-1998; 98US-0100627P.

PR 16-SEP-1998; 98US-0100661P.

PR 16-SEP-1998; 98US-0100662P.

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PR 17-SEP-1998; 98US-0100684P.

PR 17-SEP-1998; 98US-0100710P.

PR 17-SEP-1998; 98US-0100711P.

PR 17-SEP-1998; 98US-0100919P.

PR 17-SEP-1998; 98US-0100930P.

PR 18-SEP-1998; 98US-0100849P.

PR 18-SEP-1998; 98US-0100849P.

PR 18-SEP-1998; 98US-0101044P.

PR 18-SEP-1998; 98US-0101066P.

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PR 23-SEP-1998; 98US-0101476P.

PR 23-SEP-1998; 98US-0101477P.

PR 23-SEP-1998; 98US-0101479P.

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PR 06-OCT-1998; 98US-0103449P.

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PR 29-OCT-1998; 98US-0106384P.

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PR 03-NOV-1998; 98US-0106856P.

PR 03-NOV-1998; 98US-0106902P.

PR 03-NOV-1998; 98US-0106905P.

PR 03-NOV-1998; 98US-0106919P.

PR 03-NOV-1998; 98US-0106932P.

PR 03-NOV-1998; 98US-0106934P.

PR 10-NOV-1998; 98US-0107783P.

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PR 17-NOV-1998; 98US-0108779P.

PR 17-NOV-1998; 98US-0108787P.

PR 17-NOV-1998; 98US-0108788P.

PR 17-NOV-1998; 98US-0108801P.

PR 17-NOV-1998; 98US-0108802P.

PR 17-NOV-1998; 98US-0108806P.

PR 17-NOV-1998; 98US-0108807P.

PR 17-NOV-1998; 98US-0108867P.

PR 17-NOV-1998; 98US-0108925P.

PR 18-NOV-1998; 98US-0108848P.

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PR 18-NOV-1998; 98US-0108850P.
 PR 18-NOV-1998; 98US-0108851P.
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 PR 22-DEC-1998; 98US-00218517.
 PR 22-DEC-1998; 98US-0113296P.
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 PR 05-JAN-1999; 99WO-US000106.
 PR 12-APR-1999; 99US-00284291.
 PR 16-APR-1999; 99US-0129674P.
 PR 23-JUN-1999; 99US-0141037P.
 PR 20-JUL-1999; 99US-0144758P.
 PR 26-JUL-1999; 99US-0145698P.
 PR 01-SEP-1999; 99WO-US020111.
 PR 15-SEP-1999; 99WO-US021194.
 PR 18-OCT-1999; 99US-00403297.
 PR 29-OCT-1999; 99US-0162506P.
 PR 30-NOV-1999; 99WO-US028313.
 PR 02-DEC-1999; 99WO-US028551.
 PR 16-DEC-1999; 99WO-US030095.
 PR 05-JAN-2000; 2000WO-US000219.
 PR 06-JAN-2000; 2000WO-US000376.
 PR 11-FEB-2000; 2000WO-US003565.
 PR 18-FEB-2000; 2000WO-US004342.
 PR 24-FEB-2000; 2000WO-US005004.
 PR 02-MAR-2000; 2000WO-US005841.
 PR 15-MAR-2000; 2000WO-US006884.
 PR 17-MAY-2000; 2000WO-US013705.
 PR 22-MAY-2000; 2000WO-US014042.
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 PR 23-AUG-2000; 2000WO-US023522.
 PR 24-AUG-2000; 2000WO-US023328.
 PR 08-NOV-2000; 2000WO-US030952.
 PR 10-NOV-2000; 2000WO-US030873.
 PR 01-DEC-2000; 2000WO-US032678.
 PR 28-FEB-2001; 2001WO-US006520.
 PR 01-MAR-2001; 2001WO-US006666.
 PR 01-JUN-2001; 2001US-00872035.
 PR 01-JUN-2001; 2001WO-US017800.
 PR 14-JUN-2001; 2001US-00892636.
 PR 20-JUN-2001; 2001WO-US019692.
 PR 29-JUN-2001; 2001WO-US021066.
 PR 09-JUL-2001; 2001WO-US021735.
 PR 04-SEP-2001; 2001US-00946374.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Baker KP, Botstein D, Desnoyers L, Eaton DL, Ferrara N, Fong S;
 PI Gao W, Goddard A, Godowski P, Grimaldi JC, Gurney AL, Hillan KJ;
 PI Fan J, Paoni NF, Roy MA, Smith V, Stewart TA, Tumas D, Watanabe CK;
 PI Williams PW, Wood WI;
 XX
 DR WPI: 2003-765413/72.
 DR P-PSDB; ADE50090.
 XX
 PT Novel isolated PRO polypeptides useful for tissue typing, modulating
 PT biological activity of cell, as molecular weight markers in protein
 Query Match 87.3%; Score 3060.8; DB 9; Length 3143;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 3062; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 173 AGAGTCCCTGGTGACAGTCTGTGGCTGAGCATGGCCCTCCAGCCCTGGGCTGGACCC 232
 DB 74 AGAGTCCCTGGTGACAGTCTGTGGCTGAGCATGGCCCTCCAGCCCTGGGCTGGACCC 133
 QY 233 CTGGAGCCCTCCCTGGGCTTTTCTCTTCCAACTGCTTCAGCTGTGCTGCCGACGACAC 292
 DB 134 CTGGAGCCCTCCCTGGGCTTTTCTCTTCCAACTGCTTCAGCTGTGCTGCCGACGACAC 193
 QY 293 CGCGGGGGAGGGCGGCGAGGGGCCCATGCCAGGGGTTCAGATATCTATGCGAGGGATGAACG 352

DB 194 CGCGGGGGAGGGCGGCGAGGGGCCCATGCCAGGGTTCAGATATCTATGCGAGGGATGAACG 253
 QY 353 TAGGGCACCTAGCTTCTTCCACAGAAAGGCTCCAGAGTTTGTGACACTCTCTCTGAG 412
 DB 254 TAGGGCACCTAGCTTCTTCCACAGAAAGGCTCCAGGATTTTGACACTCTCTCTGAG 313
 QY 413 TGGTGATGGAATATCTCTTCTAGTGGGGCTCGAAGGCAATCTGGCCCTGGATATCCA 472
 DB 314 TGGTGATGGAATATCTCTCTAGTGGGGCTCGAAGGCAATCTGGCCCTGGATATCCA 373
 QY 473 GGATCCAGGGGTCCCGAGGCTAAAGAAATGATACCGTGGCCAGCCAGTGAAGAAAAA 532
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 QY 533 GAGTGAATGTGCTTTTAAAGAAAGCAATGAGACACAGTGTTCATCTCATCTCGTGT 592
 DB 434 GAGTGAATGTGCTTTTAAAGAAAGCAATGAGACACAGTGTTCATCTCATCTCGTGT 493
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 DB 494 CTTGGTTTCTTCAATGTCAACCATCTCTACACCTTGGCGGCACTTCCGCTTCAGCCCTGC 553
 QY 653 TTGTACTCTTCAATGAATCTTCAAGATCTTCACTGTTCCTTGGCCATCTCGAGGACAAGTCA 712
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 QY 953 AGCAGGAGTTGACTTCTTTGAGAGGCTCCACATCGGGGTGGCTAGAGTCTGCA 1012
 DB 854 AGCAGGAGTTGACTTCTTTGAGAGGCTCCACATCGGGGTGGCTAGAGTCTGCA 913
 QY 1013 GAATGACGTGGGCGGAAAAAGCTGTGAGAAAGTGGACACCTTCTTGAAGGCCCA 1072
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: April 24, 2004, 23:54:27 ; Search time 9229.41 Seconds
(without alignments)
16460.143 Million cell updates/sec

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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	3288.4	92.1	3257	9	BC020974	Homo sapi
2	3060.8	87.3	3143	6	AX697208	Sequence
3	3060.8	87.3	3143	9	AY358531	Homo sapi
4	3043.8	86.8	3252	9	AB029394	Homo sapi
5	3031.4	86.5	3151	6	BD249136	27 human
6	3008.8	86.5	3151	9	HSM807023	Homo sapi
7	2682.2	76.5	2981	6	AX746734	Sequence
8	2682.2	76.5	2981	9	AK091127	Homo sapi
9	2642.8	75.4	2768	6	AX512887	Sequence
10	2279.4	65.0	2281	6	AX528271	Sequence
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15	1771.2	50.5	3159	10	BC025800	Mus muscu
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25	486.6	13.9	249206	2	AC145168	Mus muscu
26	470	13.4	988	6	AX430331	Sequence
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28	436.4	12.5	246036	2	AC097816	Rattus no
29	436.4	12.5	289877	2	AC119762	Rattus no
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38	262.6	7.5	3781	6	AX697184	Sequence
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45	236.6	6.8	2156	6	AX060313	Sequence

ALIGNMENTS

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LOCUS
DEFINITION Homo sapiens hypothetical protein FLJ12287 similar to semaphorins,
mRNA (cdna clone MGC:9542 IMAGE:3847802), complete cds.
ACCESSION BC020974
VERSION BC020974.1 GI:18088092
KEYWORDS MGC.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 3257)
AUTHORS Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,

Pred. No. is the number of results predicted by chance to have a

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Db 781 CTGGTACTATGAACAACACTTCTGGGAGTGAAGCCATCTCTGATGCGACACTGGGATCCC 840
QY 847 AGCCTGTCTCTAAGACGACAACTTCTCCGCTGGCTGCATCATGACGCTCTCTTTGG 906
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AUTHORS	Ferrara,N., Stewart,T.A., Williams,P.M., Baker,K.P., Desnoyers,L., Eaton,D.L., Gao,W.Q., Pan,J., Botstein,D., Fong,S., Goddard,A., Godowski,P.J., Gurney,A.L., Smith,V., Tumas,D., Wood,W.I., Grimaldi,C.J., Hillan,K.J., Paoni,N.F., Roy,M.A. and Watanabe,C.K.							
TITLE	Secreted and transmembrane polypeptides and nucleic acids encoding the same							
JOURNAL	Patent: WO 0078961-A 276 28-DEC-2000;							
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Query Match 87.3%; Score 3060.8; DB 6; Length 3143;								
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QY	293	CGCGGGGGAGCGGGCAGGGGCCCATGGCCAGGTCAGATCTATCGAGGGATGAACG	352					
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VERSION AY358531.1 GI:37182184
KEYWORDS FLI_CDNA.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 3143)
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Clark, H.F., Gurney, A.L., Abaya, E., Baker, K., Baldwin, D., Brush, J., Chen, J., Chow, B., Chui, C., Crowley, C., Currell, B., Deuel, B., Dowd, P., Eaton, D., Foster, J., Grimaldi, C., Gu, Q., Hass, P.E., Heldens, S., Huang, A., Kim, H.S., Klimowski, L., Jin, Y., Johnson, S., Lee, J., Lewis, L., Liao, D., Mark, M., Robbie, E., Sanchez, C., Schoenfeld, J., Seshagiri, S., Simmons, L., Singh, J., Smith, V., Stinson, J., Vagts, A., Vanden, R., Watanabe, C., Weiland, D., Woods, K., Xie, M.H., Yansura, D., Yi, S., Yu, G., Yuan, J., Zhang, M., Zhang, Z., Goddard, A., Wood, W.I., and Godowski, P.
TITLE The Secreted Protein Discovery Initiative (SPDI), a Large-Scale Effort to Identify Novel Human Secreted and Transmembrane Proteins: A Bioinformatics Assessment
JOURNAL Genome Res. 13 (10), 2265-2270 (2003)
PUBMED 12975309
REFERENCE 2 (bases 1 to 3143)
AUTHORS Clark, H.F.
TITLE Direct Submission

JOURNAL Submitted (01-AUG-2003) Department of Bioinformatics, Genentech,
Inc., 1 DNA Way, South San Francisco, CA 94080, USA
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ORIGIN

Query Match 87.3%; Score 3060.8; DB 9; Length 3143;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 3062; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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ORIGIN

Query Match 86.8%; Score 3043.8; DB 9; Length 3252;
Best Local Similarity 99.4%; Pred. No. 0;
Matches 3077; Conservative 0; Mismatches 17; Indels 3; Gaps 2;

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DB	2136	GCCAGGACAGACCTGCGCTGGAATCTGAACTTGGCAGGCACTCCCGGGGAGCATGTGA	2195


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VERSION BD249136.1 GI:33058906
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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PD 19-NOV-2002 JP 200605787
PF 16-MAR-2000 JP 200605787
PR 18-MAR-1999 US 60/125055
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A ROSEN, YANGGU SHI,
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DEFINITION Sequence 319 from Patent EP1308459.
ACCESSION AX746794
VERSION AX746794.1 GI:32131182
KEYWORDS
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ORGANISM Homo sapiens
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Isogai,T., Sugiyama,T., Otsuki,T., Wakamatsu,A., Sato,H., Ishii,S., Yamamoto,J.I., Isono,Y., Hio,Y., Otsuka,K., Nagai,K., Irie,R., Tamechika,I., Seki,N., Yoshikawa,T., Otsuka,M., Nagahara,K. and Masuho,Y.
Full-length cDNA sequences
Patent: EP 1308459-A 319 07-MAY-2003;
Helix Research Institute (JP) ; Research Association for Biotechnology (JP)
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Db	2967	AAAAATATAAGGCTT 2981	
RESULT 8			
AK091127			
LOCUS			
DEFINITION	AK091127	2981 bp	linear
	Homo sapiens cDNA FLJ33808 fis, clone CTONG2001749, highly similar to SEMAPHORIN 4A PRECURSOR.		
ACCESSION	AK091127		
VERSION	AK091127.1	GI:21749423	
KEYWORDS	oligo capping; fis (full insert sequence).		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
REFERENCE			
AUTHORS			
	Nishi,T., Ota,T., Nakagawa,S., Senoh,A., Mizuguchi,H., Inagaki,H., Sugiyama,T., Irie,R., Otsuki,T., Sato,H., Wakamatsu,A., Ishii,S., Yamamoto,J., Isono,Y., Kawai-Hio,Y., Saito,K., Nishikawa,T., Kimura,K., Yamashita,H., Matsuo,K., Nakamura,Y., Sekine,M., Kikuchi,H., Kanda,K., Wagatsuma,M., Murakawa,K., Kanehori,K., Takahashi-Fujii,A., Oshima,A., Sugiyama,A., Kawakami,B., Suzuki,Y., Sugano,S., Naganari,K., Masuno,Y., Nagai,K. and Isegai,T.		
TITLE	NEDO human cDNA sequencing project		
JOURNAL	Unpublished		

REFERENCE 2 (bases 1 to 2981)
AUTHORS Isogai, T. and Yamamoto, J.
TITLE Direct Submission
JOURNAL Submitted (04-JUN-2002) Takao Isogai, FLJ Project (HRI Team); 2-6-7
Kazusa-Kamatari, Kisarazu, Chiba 292-0812, Japan
(E-mail: genomics@hri.co.jp, Tel: 81-438-52-3975, Fax: 81-438-52-3986)
COMMENT NEDO human cDNA sequencing project supported by Ministry of
Economy, Trade and Industry of Japan; cDNA full insert sequencing:
Research Association for Biotechnology (RAB); cDNA library
construction: Helix Research Institute (HRI) (supported by Japan
Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB,
HRI, and Biotechnology Center, National Institute of Technology and
Evaluation; clone selection for full insert sequencing: HRI and
RAB; annotation: HRI and RAB.
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/clone_lib="CTONG2"
/note="cloning vector: pME18SFL3"
ORIGIN
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Best Local Similarity 96.5%; Pred. No. 0;
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DB 186 AGGGATGAACCTAGGACCTTAGCTCTTCCACAGAGGCGCTCCAGGATTTTGACAC 245
QY 401 TCTGCTCTGAGTGTGATGGAATACCTCTACGTGGGGGCTCGAAGGCATTTCTGGC 460
DB 246 TCTGCTCTGAGTGTGATGGAATACCTCTACGTGGGGGCTCGAAGGCATTTCTGGC 305
QY 461 CTTGGATATCCAGGATCCAGGGGTCCTCCAGGCTTAAGAACATGATACCTGGCCAGCCAG 520
DB 306 CTTGGATATCCAGGATCCAGGGGTCCTCCAGGCTTAAGAACATGATACCTGGCCAGCCAG 365
QY 521 TGACAGAAAAAGAGTAATGTGCTTTAAGAAAGAGCAATGAGACACAGTGTTCAA 580
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QY 581 CTTATCCCGTCTCTGGTTCTTACAAATGTACCCCATCTCTACACCTGGGACCTTCGC 640
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DB 1407 AGGAGTGTCTGAGGAGTGGCGGAGCCCGAGCCAACTGTAGTGTCTATGAGAGTGTGTGAGCTG 1466
QY 1721 TGTCTTGGCGGAGCCCGCAGTGTGCTGGAGCCCTGAGTCCCGAACTGTGTGCTCCT 1780
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DB 1527 GTCTGCCCCCAACTGAACTCTTGAAGCAGGACATGGAGCGGGGAAACCCAGAGTGGGC 1586
QY 1841 ATGTGCGAGTGGCCCCATGAGCAGGAGCCCTTGGGCTCTGAGCGCGCCCGCAATCATTA 1900
DB 1587 ATGTGCGAGTGGCCCCATGAGCAGGAGCCCTTGGGCTCTGAGCGCGCCCGCAATCATTA 1646
QY 1901 AGAAGTCTCTGGCTGTCCCTAACTCTCTGAGTCTCCCTGCGCCCGCAGCTGTGAGCT 1960
DB 1647 AGAAGTCTCTGGCTGTCCCTAACTCTCTGAGTCTCCCTGCGCCCGCAGCTGTGAGCT 1706
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Qy	2201	CAGGTCAGTGTGGGGCGCCCTGGCTGGCCAGCAGTCTCTACTGGGCCCACTTTGTCAC	2260
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Db	2127	GAAGGCCCGGTTAAGCAGAGAGCAACACCTCCAGTCTCTCCCAAGGAATGCAGGACCTGTGC	2186
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Db	2427	CCCTTTACCAAGCACATGAGCTCTCTAAACAGGGTGAGGGGTACCCCCAGACACCTGTCTCT	2486
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Qy	3041	CACCTTTCTTCTGTGCTTGGGGCAGACCTCTGATCCCTTCTGTCCCTGTGCAGAAATGGC	3100
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Db	2967	AAAAATATAAGGCTT 2981	
<p>RESULT 9</p> <p>AX512887</p> <p>LOCUS</p> <p>DEFINITION Sequence 35 from Patent WO02062841.</p> <p>ACCESSION AX512887</p> <p>VERSION AX512887.1 GI:233504046</p> <p>KEYWORDS</p> <p>SOURCE Homo sapiens (human)</p> <p>ORGANISM Homo sapiens</p> <p>REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.</p> <p>AUTHORS Tang, T.Y., Yue, H., Gandhi, A.R., Yao, M.G., Warren, B.A., Ding, L., Duggan, B.M., Xu, Y., Yang, J., Thangavelu, K., Lal, P.G., Honchell, C.D., Wallia, N.K., Lee, S., Lee, E.A., Richardson, T.W., Boughn, M.R. and Elliott, V.S.</p> <p>TITLE Secreted proteins</p> <p>JOURNAL Patent: WO 02062841-A 35 15-AUG-2002;</p> <p>FEATURES</p> <p>source location/Qualifiers</p> <p>1. 2768</p> <p>/organism="Homo sapiens"</p> <p>/mol_type="unassigned DNA"</p> <p>/db_xref="taxon:9606"</p> <p>/note="Incyte ID No: 7487507CB1"</p> <p>ORIGIN</p> <p>Query Match 75.4%; Score 2642.8; DB 6; Length 2768;</p> <p>Best Local Similarity 96.7%; Pred. No. 0;</p> <p>Matches 2747; Conservative 0; Mismatches 2; Indels 93; Gaps 1;</p>			
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Qy	65	CCCTGCTCTGGGGCTGGAAACCCCTTCCTTTCTCTCCTCAATGGCACCCCGCCCT	124
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Qy	125	AGAATCCAGACACCGAGTATTTCCCACTGTGGCTGGTTCAAGGGTATGTGAGAGCTCCCTGG	184
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Qy	185	TGACAGTCTGTGCTGAGCATGCGCTCCAGCCCTGGGCTGGACCCCTGGAGCCTCTCT	244
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Qy	245	GGGCTTTTCTCTTCCAACTGTTCCAGTGTGCTGTCGCGACGACACCGCGGGGGAGG	304
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Qy	305	CGGGCAGGGGCCCATGCCCCAGGGTCAAGTACTATGAGGGGGATGAGTAGGCACCTTAG	364
Db	301	CGGGCAGGGGCCCATGCCCCAGGGTCAAGTACTATGAGGGGGATGAGTAGGCACCTTAG	360
Qy	365	CTTCTTCCACGAGAAGGCTCCAGGATTTTGACACTGTGCTCCTGAGTGGTGATGGAAA	424
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Qy	425	TACTCTCTAGTGGGGCTCGAGAGCCATTCCTGGCTTGGGATATCCAGGATCCAGGGGT	484
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QY	665	TGAATCTCAAGATTCTTACCTGTTCGCCATCTCGGAGGACAAGGTCAATGAGGGAAGG	724
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DB	1021	CGGCGAAAAGCTGTCTGCAGAAAGTGGACCACTTCCTGAAGGCCAGGTCTCTGCAC	1080
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DB	1441	GTATACCGGTTGAGTGGAGACAGCCAGGGCTTTGATGGGCACAGCCATCTTGTTCAT	1500
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DB	1540	-----	1539

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DB	1540	-----GGGTGCAGTGTTTGTAGGCTTCTCAGAGAGTGTCGTGAGAGGGTGCCCGC	1597
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DB	1588	AGCCAACTGTAGTGTCTATCAGAGAGCTGTGTGGACTGTGTCTTGTCCCGGAGACCCCCACTG	1647
QY	1745	TGCTTGGGACCCGTAGTCCGAACTGTTCCTTCCTGTCTGTGCCCCCMAACTGTGAATCTCTG	1804
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QY	1805	GAGCAGGACATGAGAGCGGGGGAAACCCAGAGTGGGCAATGTGCCAGTGGGCCCCCATGAGCAG	1864
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DB	1768	GAGCTTTGGCCTCAGAGCCGCCCGCAAAATCATTAAGAAAGTCCTGGCTGTCCCTAACTC	1827
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DB	1828	CACTCTGAGCTCCCTTGGCCCCCACCTGTGAGCCTTTGGCCCTTATTTATTTGGAGTCATGG	1887
QY	1985	CCAGCAGCAGTCCCAAGAGCCTTTCCACTGTCTACAATGGTCCCTCTTTGTGTAGT	2044
DB	1988	CCAGCAGCAGTCCCAAGAGCCTTTCCACTGTCTACAATGGTCCCTCTTTGTGTAGT	1947
QY	2045	GCAGGATGAGATTTGGGGGTCTTACAGTGTCTGGGCAACTGAGNATGGCTTTTCATACCC	2104
DB	1948	GCAGGATGAGATTTGGGGGTCTTACAGTGTCTGGGCAACTGAGNATGGCTTTTCATACCC	2007
QY	2105	TGTGATCTCTACTTGGGTGGACAGCCAGGACCCAGACCCCTGGCCCTGTGATCCTGAACTGGC	2164
DB	2008	TGTGATCTCTACTTGGGTGGACAGCCAGGACCCAGACCCCTGGCCCTGTGATCCTGAACTGGC	2067
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DEFINITION Sequence 9 from Patent W00206339.
ACCESSION AX528271
VERSION AX528271.1 GI:25172573
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Spaderna,S.K., Tchernev,V., Liu,X., Shenoy,S., Spytek,K.,
Zerhusen,B., Patturajan,M., Taupier,R.J., Rastelli,L., Grosse,W.M.,
Szekeres,E.S., Alsobrook,J.I., Lepley,D.M., Shen,L., Burgess,C.E.,
Shimkets,R.A. and Padigaru,M.
TITLE Proteins and nucleic acids encoding same
JOURNAL Patent: WO 0206339-A 9 24-JAN-2002;
Curagen Corporation (US)
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LOCUS 2271 bp DNA linear PAT 21-NOV-2002
DEFINITION Sequence 7 from Patent WO0206339.
ACCESSION AX528269
VERSION AX528269.1 GI:25172572
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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REFERENCE
AUTHORS Spaderina, S.K., Tchernev, V., Liu, X., Shenoy, S., Spytek, K.,
Zerhusen, B., Patturajan, M., Taupier, R.J., Rastelli, L., Grosse, W.M.,
Szekeres, E.S., Alsobrook, J.I., Lepley, D.M., Shen, L., Burgess, C.E.,
Shinkets, R.A. and Padigaru, M.
TITLE Proteins and nucleic acids encoding same
JOURNAL Patent: WO 0206339-A 7 24-JAN-2002;
Curagen Corporation (US)
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VERSION AX879068.1 GI:40033804
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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Ota, T., Isogai, T., Nishikawa, T., Hayashi, K., Saito, K., Yamamoto, J.,
Ishii, S., Sugiyama, T., Wakamatsu, A., Nagai, K. and Otsuki, T.
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Research Association for Biotechnology (JP)
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LOCUS	BD157628	1838 bp	DNA linear
DEFINITION	Primer for synthesizing full-length CDNA and use thereof.		PAT 17-JAN-2003
ACCESSION	BD157628.1		GI:27863386
VERSION	JP 2002191363-A/12471.		
KEYWORDS	Homo sapiens (human)		
SOURCE	Homo sapiens		
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.		
REFERENCE	1 (bases 1 to 1838)		
AUTHORS	Ota,T., Isogai,T., Nishikawa,T., Hayashi,K., Saito,K., Yamamoto,J., Ishii,S., Sugiyama,T., Wakamatsu,A., Nagai,K. and Otsuki,T.		
TITLE	Primer for synthesizing full-length CDNA and use thereof		
JOURNAL	Patent: JP 2002191363-A 12471 09-JUL-2002;		
COMMENT	HELIX RESEARCH INSTITUTE OS Homo sapiens (human) FN JP 2002191363-A/12471 PD 09-JUL-2002 PF 28-JUL-2000 JP 2000280990 PI TOSHIO OTA,TAKAO ISOGAI,TETSUO NISHIKAWA,KOJI HAYASHI,KAORU SAITO, PI JUNICHI YAMAMOTO,SHIZUKO ISHII,TOMOYASU SUGIYAMA,AI WAKAMATSU, PI KEIICHI NAGAI,TETSUJI OTSUKI PC C12N15/09,C07K14/47,C07K16/18,C12N1/15,C12N1/19,C12N1/21,C12N5/PC 10, PC C12P21/02,C12Q1/68//C12P21/08,G06F17/30,C12N15/00,C12N5/00 CC Primer for synthesizing full-length CDNA and use thereof FH Key FT CDS Location/Qualifiers 1..1838 Location/Qualifiers		
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Matches 1838; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
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RESULT 14
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AK022349
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 Isogai, T., Ota, T., Hayashi, K., Sugiyama, T., Otsuki, T., Suzuki, Y., Nishikawa, T., Nagai, K., Sugano, S., Shiratori, A., Sudo, H., Wagatsuma, M., Hosouri, T., Kaku, Y., Kodaira, H., Kondo, H., Sugawara, M., Takahashi, M., Chiba, Y., Ishida, S., Murakawa, K., Ono, Y., Takiguchi, S., Watanabe, S., Kimura, K., Murakami, K., Ishii, S., Kawai, Y., Saito, K., Yamamoto, J., Wakamatsu, A., Nakamura, Y., Nagahari, K., Masuho, Y., Ninomiya, K. and Iwayanagi, T. NEDO human cDNA sequencing project
Unpublished
2 (bases 1 to 1838).
Isogai, T. and Otsuki, T.
Direct Submission
Submitted (23-AUG-2000) Takao Isogai, Helix Research Institute, Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan (E-mail: genomics@hri.co.jp, Tel: 81-438-52-3975, Fax: 81-438-52-3986)
NEDO human cDNA sequencing project supported by Ministry of International Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology; cDNA library construction, 5'- and 3'-end one pass sequencing and clone selection: Helix Research Institute (supported by Japan Key Technology Center etc.) and Department of Virology, Institute of Medical Science, University of Tokyo.
FEATURES
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GenCore version 5.1.6
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Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum Match 100%

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

EST:

1: em_estba.*

2: em_esthum.*

3: em_estin.*

4: em_estmu.*

5: em_estov.*

6: em_estpl.*

7: em_estro.*

8: em_htc.*

9: gb_est1.*

10: gb_est2.*

11: gb_htc.*

12: gb_est3.*

13: gb_est4.*

14: gb_est5.*

15: em_estfun.*

16: em_estcom.*

17: em_ges_hum.*

18: em_ges_inv.*

19: em_ges_pln.*

20: em_ges_vrt.*

21: em_ges_fun.*

22: em_ges_nam.*

23: em_ges_mus.*

24: em_ges_pro.*

25: em_ges_rod.*

26: em_ges_phg.*

27: em_ges_vrl.*

28: gb_gse1.*

29: gb_gse2.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	792.6	99.1	861	13	BUI93627
2	777.4	97.2	978	13	BUI540102
3	775.4	96.9	821	13	BUI94796
4	719.6	90.0	816	12	BI770798

ALIGNMENTS

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RESULT 1
BUI93627
LOCUS      AGENCOURT_7905281 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:6160888
DEFINITION 5', mRNA sequence.
ACCESSION  BUI93627
VERSION    BUI93627.1 GI:22707611
KEYWORDS   EST.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE  1 (bases 1 to 861)
            NIH-MGC http://mgi.nci.nih.gov/.
AUTHORS   National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE     Unpublished (1999)
JOURNAL   Contact: Robert Strausberg, Ph.D.
COMMENT   Email: cgabbs-remail.nih.gov
            Tissue Procurement: ATCC/DCTD/PTP
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Agencourt Bioscience Corporation
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAMI3512 row: e column: 17
            High quality sequence stop: 692.

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5 702.6 87.8 903 12 BI768969
6 663 82.9 705 14 CA419320
7 627.4 78.4 963 10 BE893633
8 623.8 78.0 990 12 BQ20473
9 613 76.6 653 12 BI460396
10 611.8 76.5 660 12 BM998183
11 611.2 76.4 642 12 BM761296
12 605.4 75.7 696 9 AV700754
13 605.4 75.0 832 13 BU940543
14 599.6 75.0 946 12 BI552760
15 587.2 73.4 946 14 CA419457
16 560.2 70.0 740 13 BU942323
17 529.6 66.2 578 12 BM984608
18 517.4 64.7 727 12 BG527549
19 484.4 60.5 584 12 BI827304
20 455.8 57.0 745 12 BI549606
21 432 54.0 454 9 AA757285
22 414.8 51.8 418 9 AI355317
23 413.2 51.6 455 12 BM782882
24 412 51.5 954 13 BU595224
25 404.6 50.6 427 9 AA865734
26 396.4 49.5 433 9 AW102885
27 372 46.5 486 9 AI581344
28 343.2 42.9 583 12 BG718159
29 340.4 42.5 415 9 AV695928
30 243 30.4 289 10 BF751332
31 222.4 27.8 352 9 AV696887
32 208.2 26.0 867 12 BG680761
33 193.6 24.2 704 12 BM826625
34 190.4 23.8 709 14 CB438378
35 187.6 23.4 930 13 BX350756
36 186.2 23.3 2508 29 AV398883
37 178.4 22.3 696 12 BQ044923
38 173.6 21.7 881 13 BQ880096
39 166 20.8 605 14 CB162968
40 166 20.8 949 14 CD108543
41 163.2 20.4 3767 11 AK083942
42 162.8 20.4 508 12 BI712887
43 157.6 19.7 2508 29 AV398885
44 156.8 19.6 808 14 CB238339
45 154.6 19.3 643 14 CF362512

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Db 790 TAAAGATGTTCTCTTTTCC 809

RESULT 2
BU540102 978 bp mRNA linear EST 13-SEP-2002
LOCUS AGENCOURT_10322115 NIH_MGC_128 Homo sapiens cDNA clone
DEFINITION IMAGE:6571438 5', mRNA sequence.
BU540102
ACCESSION BU540102.1 GI:22850543
VERSION EST. sapiens (human)
KEYWORDS Homo sapiens
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 978)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLES National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: rgs@nih.gov
Tissue Procurement: NCI
CDNA Library Preparation: Michael Brownstein Laboratory
CDNA Sequencing by: The I.M.A.G.E. Consortium (ILLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/ILLNL at:
http://image.llnl.gov
Plate: LHC2761 row: 0 column: 22
High quality sequence stop: 700.

FEATURES
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6571438"
/tissue_type="mixed (pool of 40 RNAs)"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NIH_MGC_128"
/note="Vector: pDNR-LIB; Site 1: SfiI (ggccattatggcc);
Site 2: SfiI (ggccctctggcc); Double-stranded cDNA was
prepared from a pool of 40 cell line polyA+ RNAs (bladder
- 2%, blood - 33.4%, brain - 5.6%, breast - 12.5%, colon -
4%, connective tissue - 1.4%, eye - 1%, intestine - 2.6%,
kidney - 2.2%, liver - 5.7%, lung - 10.8%, NK-cell -
5.2%, ovary - 4%, pharynx - 2.5%, prostate - 4.3%,
salivary gland - 1.3%, and skin - 2.3%). 5' and 3'
adaptors were used in cloning as follows:
5'-AAGCAGTGTATCAAGCAGTGGCCTAGCCGCGG-3' and
5'-ATTCTAGGCGGAGCGCGGCGACATG-T(30)NN-3'. Full-length
enriched library was constructed using the Clontech
Creator SMART kit and size-selected to contain the >2 kb
size fraction (other fractions present in NIH MGC 126 and
NIH MGC 127). Library created in the laboratory of T.
Usdin, M.D., Ph.D. (NIH, NIH). Note: this is a NIH_MGC
Library."

ORIGIN
Query Match 97.2%; Score 777.4; DB 13; Length 978;
Best Local Similarity 99.0%; Pred. No. 2.1e-200;
Matches 792; Conservative 0; Mismatches 7; Indels 1; Gaps 1

QY 1 CTCTCTCCAGAGGTCCAGACTTCAGGACTGAAACATGACCGATAAACAGAGAAGG 60
Db 10 CTCTCTCCAGAGGTCCAGACTTCAGGACTGAAACATGACCGATAAACAGAGAAGG 69
QY 61 TGGCTGTAGATCTGAAACCTGTTTAAACGTCCTCCAGGAAATGTGACAGTCTCTCGTATC 120
Db 70 TGGCTGTAGATCTGAAACCTGTTTAAACGTCCTCCAGGAAATGTGACAGTCTCTCGTATC 129
QY 121 AGAAAGGCGAGAGTATGCGCCCTGTTGGCAAGGAAACAGGAGGAGAGACGCTTATG 180
Db 130 AGAAAGGCGAGAGTATGCGCCCTGTTGGCAAGGAAACAGGAGGAGAGACGCTTATG 189
QY 181 CAGCTCTGCATGCTCCAAAGAAAGAGCTTATGACGAGCATGCTATTCACCCAGCC 240
Db 190 CAGCTCTGCATGCTCCAAAGAAAGAGCTTATGACGAGCATGCTATTCACCCAGCC 249
QY 241 AATTGGATTCTCAGATTGATGATTCACGTGTTTACGAAAGATAGGATGATGAGAAC 300
Db 250 AATTGGATTCTCAGATTGATGATTCACGTGTTTACGAAAGATAGGATGATGAGAAC 309
QY 301 CTGCTAGCAATGACCTCTGGAGGAAACCTTACGACGAGTTTCTCTGAGATGACCTAG 360
Db 310 CTGCTAGCAATGACCTCTGGAGGAAACCTTACGACGAGTTTCTCTGAGATGACCTAG 369
QY 361 AATCAGAGAAACAGGCTCTCTCCCAAGGCAAGAGAAATTAATGCTGATNTAAAC 420
Db 370 AATCAGAGAAACAGGCTCTCTCCCAAGGCAAGAGAAATTAATGCTGATNTAAAC 429
QY 421 GTAATTTAGTGAAGAACTCCGATGCTTGGACAAAATATGAAAAATCTCGAAATGC 480
Db 430 GTAATTTAGTGAAGAACTCCGATGCTTGGACAAAATATGAAAAATCTCGAAATGC 489
QY 481 TTGAAGAGTGAAGAACTTCTGAGTCAAGAGGATTTTGAATCATCATCAAGG 540
Db 490 TTGAAGAGTGAAGAACTTCTGAGTCAAGAGGATTTTGAATCATCATCAAGG 549
QY 541 AAGCAGCAAGATGATCAGAGGACCTTCTTAAGACCTTAAAGAAACTGAAACGTA 600
Db 550 AAGCAGCAAGATGATCAGAGGACCTTCTTAAGACCTTAAAGAAACTGAAACGTA 609
QY 601 TGATTTGAGAAATCTGTCCTGAGGAAATATCACCACCAATATGATATCTCGTTAT 560
Db 610 TGATTTGAGAAATCTGTCCTGAGGAAATATCACCACCAATATGATATCTCGTTAT 569
QY 661 GATTGAGAGAGAAAGATCAGATTCCTGTTTCTACATGAGCAGGATATGCTGAA 720
Db 670 GATTGAGAGAGAAAGATCAGATTCCTGTTTCTACATGAGCAGGATATGCTGAA 729
QY 721 GTCTCTTGGCATATGTTACCGAATCAATAGCCCTCCAGAGGCTAAGAAATTTCTGTTAG 780
Db 730 GTCTCTTGGCATATGTTACCGAATCAATAGCCCTCCAGAGGCTAAGAAATTTCTGTTAG 789
QY 781 TAAAGATGTTCTTTTCCC 800

QY	181	CAGGCTGCCATGTCCTCCAAAGAAAGAGCTTATGACAGGACATGCTATTCCACCAGGCC	240
Db	207	CAGGCTGCCATGTCCTCCAAAGAAAGAGCTTATGACAGGACATGCTATTCCACCAGGCC	266
QY	241	AATTGGATTCTCAGATTGATGACCTTCATCTGCTTTTTCAGCAAGATAGATGATGAGAAAC	300
Db	267	AATTGGATTCTCAGATTGATGACCTTCATCTGCTTTTTCAGCAAGATAGATGATGAGAAAC	326
QY	301	CTGGTAGCAATGACCTCTGGGAGGAAAGCTTACCAGAGATTTCTCTGGAGATGACCTAG	360
Db	327	CTGGTAGCAATGACCTCTGGGAGGAAAGCTTACCAGAGATTTCTCTGGAGATGACCTAG	386
QY	361	AATGACAGAAACAGCTCTCTCCAAAGCAACAGAGAAATTAATGCTGATATAAAC	420
Db	387	AATGACAGAAACAGCTCTCTCCAAAGCAACAGAGAAATTAATGCTGATATAAAC	446
QY	421	GTAATTTAGTGAAGAACTCCGATCGTTGGACAAATATGAAAAATCTTCGAATGC	480
Db	447	GTAATTTAGTGAAGAACTCCGATCGTTGGACAAATATGAAAAATCTTCGAATGC	506
QY	481	TTGAAGGAGTGCAAGACCTACTGCAAGTCAAGAAAGCGATTTTGAATCCATCAAGG	540
Db	507	TTGAAGGAGTGCAAGACCTACTGCAAGTCAAGAAAGCGATTTTGAATCCATCAAGG	566
QY	541	AGCAGCAAGATGATGAGACGAGACTTTGTTAAGCCTTAAGAAAGAACTGAAACGTA	600
Db	567	AGCAGCAAGATGATGAGACGAGACTTTGTTAAGCCTTAAGAAAGAACTGAAACGTA	626
QY	601	TGATTTGAGAACTTGTCTCTGGAGGATTAATCAACCCCAAAATGCAATCTCTGTTAAT	660
Db	627	TGATTTGAGAACTTGTCTCTGGAGGATTAATCAACCCCAAAATGCAATCTCTGTTAAT	686
QY	661	GATTGAGGAGAAAGGATGATGCTGCTTTTCTAGCAATGAGCAGGATTAATGCTGAA	720
Db	687	GATTGAGGAGAAAGGATGATGCTGCTTTTCTAGCAATGAGCAGGATTAATGCTGAA	746
QY	721	GTCCTCTGCAATGTTACCGAATCAATPAG-CCTTCCAGAGGCTAAGAAATTTCTGTTA	779
Db	747	GTCCTCTGCAATGTTACCGAATCAATPAG-CCTTCCAGAGGCTAAGAAATTTCTGTTA	806
QY	780	GTAAGAAGATGTTCTTTTCC 799	
Db	807	GTAAGAAGATGTTCTTTTCC 826	
RESULT 3			
LOCUS	BU194796		
DEFINITION	AGENCOURT_7970656 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:6163541		
ACCESSION	BU194796		
VERSION	BU194796.1		
KEYWORDS	EST.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
TITLE	NIH-MGC http://mgc.nci.nih.gov/;		
JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC)		
COMMENT	Unpublished (1999)		
	Contact: Robert Strausberg, Ph.D.		
	Email: cgabbs@mail.nih.gov		
	Tissue Procurement: ATCC/DCPD/PTP		
	cDNA Library Preparation: Life Technologies, Inc.		
	DNA Sequencing by: Agencourt Bioscience Corporation		
	Clone distribution: MGC clone distribution information can be		
	found through the I.M.A.G.E. Consortium/LLNL at:		
	http://image.llnl.gov		
	Place: LLNL13519 row: d column: 06		
	High quality sequence stop: 725.		

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	/tissue_type="melanotic melanoma"
	/lab_host="DH10B (phage-resistant)"
	/clone_lib="NIH_MGC_72"
	/note="Organ: skin; Vector: pCMV-SPORT6; Site 1: NotI; Site 2: SalI; Cloned unidirectionally. Primer: Oligo.dT. Average insert size 2 kb. Library constructed by Life Technologies."
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Query Match	96.9%; Score 775.4; DB 13; Length 821;
Best Local Similarity	99.0%; Pred. No. 7e-200;
Matches 791; Conservative	0; Mismatches 6; Indels 2; Gaps 1;
QY	1 CTCTCTCCAGCAAGGTCAGGACTTCAGGACTGAAACAATGACCGATATAAACAGAGAAGG 60
Db	10 CTCTCTCTCCAGCAAGGTCAGGACTTCAGGACTGAAACAATGACCGATATAAACAGAGAAGG 69
QY	61 TGGCTGTAGATCCTGAAACTGTGTTTAAACGCTCCAGGGAATGTGACAGTCTCTTCGTATC 120
Db	70 TGGCTGTAGATCCTGAAACTGTGTTTAAACGCTCCAGGGAATGTGACAGTCTCTTCGTATC 129
QY	121 AGAAAGGAGAGGATGGCCCTGTTGGCAAGGAAACAAGGAGGAGGAGGAGGAGGAGGAGG 180
Db	130 AGAAAGGAGAGGATGGCCCTGTTGGCAAGGAAACAAGGAGGAGGAGGAGGAGGAGGAGG 189
QY	181 CAGGCTCTGCATGTCCTCAAGAAAGAAAGCTTATGACAGGACATGCTATTTCACCCAGCC 240
Db	190 CAGGCTCTGCATGTCCTCAAGAAAGAAAGCTTATGACAGGACATGCTATTTCACCCAGCC 249
QY	241 AATTGGATTTCTCAGATTGATGACTTCACTGGTTTTCAGCAAGATAGGATGATGCGAAGC 300
Db	250 AATTGGATTTCTCAGATTGATGACTTCACTGGTTTTCAGCAAGATAGGATGATGCGAAGC 309
QY	301 CTGGTAGCAATGCACTGTGGGAGGAAACGTTTACAGCAGATTTCTCTGGAGATGACCTAG 360
Db	310 CTGGTAGCAATGCACTGTGGGAGGAAACGTTTACAGCAGATTTCTCTGGAGATGACCTAG 369
QY	361 AATGCAGAGAAACAGCCTCTCTCCAAAGGCAACGAGAAATTAATGCTGATATAAAC 420
Db	370 AATGCAGAGAAACAGCCTCTCTCCAAAGGCAACGAGAAATTAATGCTGATATAAAC 429
QY	421 GTAATTTAGTGAAGAACTCCGATGCTTGGACAAAAATATGAAAAATCTTCGAAATGC 480
Db	430 GTAATTTAGTGAAGAACTCCGATGCTTGGACAAAAATATGAAAAATCTTCGAAATGC 489
QY	481 TTGAAGAGTGCAAGGACCTACTGCACTGAGGAGCGATTTTTGAATCCATCATCAAGG 540
Db	490 TTGAAGAGTGCAAGGACCTACTGCACTGAGGAGCGATTTTTGAATCCATCATCAAGG 549
QY	541 AAGCAGCAAGATGATGAGACGAGACTTTGTTAAGCAGCCTTAAGAGAAACTGAAACGTA 600
Db	550 AAGCAGCAAGATGATGAGACGAGACTTTGTTAAGCAGCCTTAAGAGAAACTGAAACGTA 609
QY	601 TGATTTGAGAAATCTTGTCTCTGGAGGATTAATCACACCCCAATGCAATATCTCGTTAAT 660
Db	610 TGATTTGAGAAATCTTGTCTCTGGAGGATTAATCACACCCCAATGCAATATCTCGTTAAT 669
QY	661 GATTGAGGAGAGAAAGGATCAGATTGCTGTTTTCTACAAATGAGGAGGATATTGCTGAA 720
Db	670 GATTGAGGAGAGAAAGGATCAGATTGCTGTTTTCTACAAATGAGGAGGATATTGCTGAA 729
QY	721 GTCCTCTGGCATATGTTTACCGAAATCAAAATAGCCTTCCAGAGGCTAA--GAAATTTCTGTT 778
Db	730 GTCCTCTGGCATATGTTTACCGAAATCAAAATAGCCTTCCAGAGGCTTAAGAAATTTCTGTT 789
QY	779 AGTAAAGATGTTCTTTTTT 797

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Db      790 AGTAAAGATGGTCTTTT 808

RESULT 4
BI770798
LOCUS   603061271F1 NIH_MGC_122 Homo sapiens cDNA clone IMAGE:5210681 5',
DEFINITION mRNA sequence.
ACCESSION BI770798.1 GI:15762376
VERSION   Homo sapiens (human)
KEYWORDS  EST.
SOURCE    Homo sapiens
ORGANISM  Homo sapiens

REFERENCE
AUTHORS  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
TITLE     Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
JOURNAL  NIH-MGC http://mgs.nci.nih.gov/.
COMMENT  National Institutes of Health, Mammalian Gene Collection (MGC)
         Unpublished (1999)
         Contact: Robert Strausberg, Ph.D.
         Email: cgabbs@mail.nih.gov
         Tissue Procurement: Life Technologies, Inc.
         cDNA Library Preparation: Life Technologies, Inc.
         DNA Sequencing by: Incyte Genomics, Inc.
         Clone distribution: MGC clone distribution information can be
         found through the I.M.A.G.E. Consortium/LLNL at:
         http://image.llnl.gov
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FEATURES
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         /clone_lib="NIH_MGC_122"
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         Site 1: NotI; Site 2: EcoRV (destroyed); RNA source
         anonymous pool of 24 week female lung, 16 week female
         spleen, and 20-22 week male spleens. Library is oligo-dT
         primed, and directionally cloned (EcoRV site is destroyed
         upon cloning). Average insert size 1.4 kb, insert size
         range 1-3 kb. Library is normalized and enriched for
         full-length clones and was constructed by C. Gruber
         (Invitrogen). Research Genetics tracking code 026. Note:
         this is a NIH_MGC Library."

ORIGIN
Query Match      90.0%; Score 719.6; DB 12; Length 816;
Best Local Similarity 98.5%; Pred. No. 1e-184;
Matches 747; Conservative 0; Mismatches 9; Indels 2; Gaps 2;

QY  44 CGATAAACAGAGAGTGCTGTAGATCTCTGAACTGTGTTTAAACGTCCTCCAGGGAATG 103
Db  1  CGATAAACAGAGAGTGCTGTAGATCTCTGAACTGTGTTTAAACGTCCTCCAGGGAATG 59
QY  104 TGACAGTCCTTCGTATCAGAAAAGGAGAGATGGCCCTGTGGCAAGGAACAAAGGAGC 163
Db  60 TGACAGTCCTTCGTATCAGAAAAGGAGAGATGGCCCTGTGGCAAGGAACAAAGGAGC 119
QY  164 AGGAGACAGCCTTATTGACAGCTCTGCCATGTCCAAAGAAAAGAAAGCTTATGACAGGACA 223
Db  120 AGGAGACAGCCTTATTGACAGCTCTGCCATGTCCAAAGAAAAGAAAGCTTATGACAGGACA 179
QY  224 TGCCTATCCACCCAGCAATGATCTCAGATTGATGATTCACCTGGTTTCAGCAAGA 283
Db  180 TGCCTATCCACCCAGCAATGATTCAGATTGATGATTCACCTGGTTTCAGCAAGA 239
QY  284 TAGGATGATCAGAAAACCTGGTAGCAATGACACCTGTGGGAGGAAACCTTACCAGCAGTTT 343
Db  240 TAGGATGATCAGAAAACCTGGTAGCAATGACACCTGTGGGAGGAAACCTTACCAGCAGTTT 299

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QY  344 CTCTGGAGATGACCTAGAAATGCAGAGAAAACAGCCTCTCTCCCAAAAGCCAAAGGAAT 403
Db  300 CTCTGGAGATGACCTAGAAATGCAGAGAAAACAGCCTCTCTCCCAAAAGCCAAAGGAAT 359
QY  404 TAATGCTGTATATAAAACGTTAAATTAAGTGAAGAACTCCGATCGTGTGGACAAAATATGA 463
Db  360 TAATGCTGTATATAAAACGTTAAATTAAGTGAAGAACTCCGATCGTGTGGACAAAATATGA 419
QY  464 AAAAATCTTCGAATGCTTGAAGAGTGCAGAGACCTACTGCACTGAGGAGGATTTT 523
Db  420 AAAAATCTTCGAATGCTTGAAGAGTGCAGAGACCTACTGCACTGAGGAGGATTTT 479
QY  524 TGAATCATCATCAAGGAAGCAGCAAGATGTATGACAGAGACTTGTGTTAAGCACCTTAA 583
Db  480 TGAATCATCATCAAGGAAGCAGCAAGATGTATGACAGAGACTTGTGTTAAGCACCTTAA 539
QY  584 GAGAAACTGAAACGATGATTTGAGAATACCTGTCCCTGGAGGATATACACCCCAA 643
Db  540 GAGAAACTGAAACGATGATTTGAGAATACCTGTCCCTGGAGGATATACACCCCAA 599
QY  644 TGCATATCTCGTTAATGATTTGAGGAGAGAAAAGGATCAGATTGCTGTGTTTCTACATGG 703
Db  600 TGCATATCTCGTTAATGATTTGAGGAGAGAAAAGGATCAGATTGCTGTGTTTCTACATGG 659
QY  704 AGCAGGATATGCTGAAGTCTCTGCGATATGTTACCGAATCAAATAGCTTCCAGAGC 763
Db  660 AGCAGGATATGCTGAAGTCTCTGCGATATGTTACCGAATCAAATAGCTTCCAGAGC 719
QY  764 TAGAAA-TTCTGTTAGTAAAGATGTTCTTTTCCC 800
Db  720 TAGAAA-TTCTGTTAGTAAAGATGTTCTTTTCCC 757

RESULT 5
BI768969
LOCUS   603058116F1 NIH_MGC_122 Homo sapiens cDNA clone IMAGE:5207667 5',
DEFINITION mRNA sequence.
ACCESSION BI768969.1 GI:15760547
VERSION   Homo sapiens (human)
KEYWORDS  EST.
SOURCE    Homo sapiens
ORGANISM  Homo sapiens
REFERENCE NIH-MGC http://mgs.nci.nih.gov/.
AUTHORS  National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE     Unpublished (1999)
JOURNAL
COMMENT   Contact: Robert Strausberg, Ph.D.
         Email: cgabbs@mail.nih.gov
         Tissue Procurement: Life Technologies, Inc.
         cDNA Library Preparation: Life Technologies, Inc.
         DNA Sequencing by: Incyte Genomics, Inc.
         Clone distribution: MGC clone distribution information can be
         found through the I.M.A.G.E. Consortium/LLNL at:
         http://image.llnl.gov
         Plate: LLAM1520 row: p column: 04
         High quality sequence stop: 804.

FEATURES
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         /notes="Organ: Pooled lung and spleen; Vector: pCMV-SPORT6;
         Site 1: NotI; Site 2: EcoRV (destroyed); RNA source
         anonymous pool of 24 week female lung, 16 week female
         spleen, and 20-22 week male spleens. Library is oligo-dT

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primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.4 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 026. Note: this is a NIH_MGC Library."

ORIGIN

Query Match 87.8%; Score 702.6; DB 12; Length 903;
Best Local Similarity 97.9%; Pred. No. 4.5e-180;
Matches 733; Conservative 0; Mismatches 14; Indels 2; Gaps 2;

QY 53 AGAAGAGTGGCTGTAGATCTGTAACCTGTTTAAACCTCCAGGAAATGTCAGATCC 112
Db 1 AGAAGAGTGGCTGTAGATCTGTAACCTGTTTAAACCTCCAGGAAATGTCAGATCC 59
QY 113 TTGCTATCAGAAAGCAGAGATGCGCTGTTGGCAAGAAACAGAGCAGAGAGACAG 172
Db 60 TTGCTATCAGAAAGCAGAGATGCGCTGTTGGCAAGAAACAGAGCAGAGAGACAG 119
QY 173 CTTTATGAGGCTTGCCATGTCCTCAAGAAAGAGCTTATGACAGGACATGCTATTCC 232
Db 120 CTTTATGAGGCTTGCCATGTCCTCAAGAAAGAGCTTATGACAGGACATGCTATTCC 179
QY 233 ACCAGCCAAATGGATCTCAGATTGATGACTTCACTGCTTTTACGAAAGATAGGATGAT 292
Db 180 ACCAGCCAAATGGATCTCAGATTGATGACTTCACTGCTTTTACGAAAGATAGGATGAT 239
QY 293 GCGAAACCTGGTAGCAATGCACTGTGGAGAAACGTTACAGCAGTTTCTCTGGAGA 352
Db 240 GCGAAACCTGGTAGCAATGCACTGTGGAGAAACGTTACAGCAGTTTCTCTGGAGA 299
QY 353 TGACCTAGAAATGAGAAACAGCCTCTCTCCAAAGCCAAAGAGAAATTAATGCTGA 412
Db 300 TGACCTAGAAATGAGAAACAGCCTCTCTCCAAAGCCAAAGAGAAATTAATGCTGA 359
QY 413 TATAAACCTAAATAGTGAAGAACTCCGATGCGTTGGACAAATAATGAAAAATCTT 472
Db 360 TATAAACCTAAATAGTGAAGAACTCCGATGCGTTGGACAAATAATGAAAAATCTT 419
QY 473 CGAAATGCTTGAGGAGTCAAGGACCTACTGCTGCTGAGAGCGATTTTGAATCCAT 532
Db 420 CGAAATGCTTGAGGAGTCAAGGACCTACTGCTGCTGAGAGCGATTTTGAATCCAT 479
QY 533 CATCAAGAGCAGCAAGATGATGAGACGAGACTTTGTTAAGCACCCTTAAGAGAAACT 592
Db 480 CATCAAGAGCAGCAAGATGATGAGACGAGACTTTGTTAAGCACCCTTAAGAGAAACT 539
QY 593 GAAACGTATGATTGAGATATCTGCTCCTGAGGATATACACCCCAATGCAATATC 652
Db 540 GAAACGTATGATTGAGATATCTGCTCCTGAGGATATACACCCCAATGCAATATC 599
QY 653 TCGTTAATGATTGAGAGAGAAAGGATCAGATTGCTGTTTCTACAATGGAGCAGGATA 712
Db 600 TCGTTAATGATTGAGAGAGAAAGGATCAGATTGCTGTTTCTACAATGGAGCAGGATA 659
QY 713 TTGCTGAAGTCTCTGGCATATGTTACCGAATCAATAGCCCTTCAGAGGCTTAAGAAAT 772
Db 660 TTGCTGAAGTCTCTGGCATATGTTACCGAATCAATAGCCCTTCAGAGGCTTAAGAAAT 719
QY 773 TCT-GTTAGTAAAGATGTTCTTTTCCC 800
Db 720 TCTGTTAGTAAAGATGTTCTTTTCCC 748

RESULT 6

CA419320/c
LOCUS
DEFINITION
UI-H-FHO-bch-o-11-0-UI.s1 NCI CGAP FHO Homo sapiens cDNA clone
UI-H-FHO-bch-o-11-0-UI 3', mRNA sequence.
ACCESSION
CA419320
VERSION
CA419320.1 GI:24781975
KEYWORDS
EST.

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (Bases 1 to 705)

NCI-CCAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Tumor Gene Index

Unpublished (1997)

Contact: Robert Strausberg, Ph.D.

Email: cgapsb@mail.nih.gov

Tissue Procurement: James Martin

cDNA Library preparation: Dr. M. Bento Soares, University of Iowa

cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa

DNA Sequencing by: Dr. M. Bento Soares, University of Iowa

Clone Distribution: Clone distribution information can be obtained

from Dr. M. Bento Soares, bento-soares@uiowa.edu

Seq primer: M13 FORWARD

POLYA-Yes

FEATURES

source

Location/Qualifiers

1..705

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="UI-H-FHO-bch-o-11-0-UI"

/tissue_type="Human Chondrosarcoma Cell Line"

/dev_stage="Adult"

/lab_host="NCI CGAP FHO"

/notes="Organ: Bone; Vector: pT73-Pac (Pharmacia) with a

modified polylinker; Site 1: EcoR I; Site 2: Not I;

NCI CGAP FHO is a cDNA library containing the following

tissue(s): Human Grade 1 Chondrosarcoma Cell Line The

library was constructed according to Bonaldo, Lennon and

Soares, Genome Research, 6:791-806, 1996. First strand

cDNA synthesis was primed with an oligo-dT primer

containing a Not I site. Double stranded cDNA was ligated

to an EcoR I adaptor, digested with Not I, and cloned

directionally into pT73-Pac vector. The oligonucleotide

used to prime the synthesis of first-strand cDNA contains

a library tag sequence that is located between the Not I

site and the (d)18 tail. The sequence tag for this

library is AGAATCCGCG. The cell line was provided by Dr

James Martin from University of Iowa

TAG TISSUE=Human Chondrosarcoma Cell Line CS8 - Grade 1

Chondrosarcoma

TAG LIB=UI-H-FHO

TAG_SEQ=AGAATCCGCG"

ORIGIN

Query Match

Best Local Similarity 97.8%; Score 663; DB 14; Length 705;

Matches 672; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

QY 112 CTTGCTATCAGAAAGCAGAGATGCGCTGTTGCAAGGAAACAGAGCAGGAGACA 171

Db 705 CTTGCTATCAGAAAGCAGAGATGCGCTGTTGCAAGGAAACAGAGCAGGAGACA 646

QY 172 GCCTTATTCAGGCTCTGCCATGTCCAAAGAAAGAGCTTATGACAGGACATGCTATTTC 231

Db 645 GCCTTATTCAGGCTCTGCCATGTCCAAAGAAAGAGCTTATGACAGGACATGCTATTTC 586

QY 232 CACCCAGCCAAATGGATTCTCAGATTGATGACTTCACTGGTTTCAGCAAGATAGGATGA 291

Db 585 CACCCAGCCAAATGGATTCTCAGATTGATGACTTCACTGGTTTCAGCAAGATAGGATGA 526

QY 292 TGCAGAAACCTGCTAGCAATGACACCTGTGGAGGAAACGTTACAGCAGTTCCTCTGGAG 351

Db 525 TGCAGAAACCTGCTAGCAATGACACCTGTGGAGGAAATGTTACAGCAATTCCTCTGGAG 466

QY 352 ATGACCTAGAAATGACAGAGAAACAGCCTCTCTCCAAAAGCCAAAGAGAAATTAATGCTG 411

Db 465 ATGACCTAGAAATGACAGAGAAATAGCCTCTCTCTCCAAAAGCCAAAGAGAAATTAATGCTG 406

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QY 412 ATATAAACGTAATTAGTGAAGAACTCCGATCGGTGGACAAAATATGAAAAATCT 471
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|
|
Db 405 ATATAAAATGTCAAGTAGTGAAGAAATCCGATCGCTTGGACGAAAATATGAAAAATCT 346
|
|
|
QY 472 TCGAAATGCTTTGAAGGAGTGCAGGACCTACTCAGTCAGGAGCGATTTTGTGATCCA 531
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|
|
Db 345 TCGAAATGCTTTGAAGGAGTGCAGGACCTACTCAGTCAGGAGCGATTTTGTGATCCA 286
|
|
|
QY 532 TCATCAAGGAGCAGCAGAGATGATGAGAGCAGACTTTGTTAAGCAGCTTTAAGAAGAAC 591
|
|
|
Db 285 TCATCAAGGAGCAGCAGAGATGATGAGAGCAGACTTTGTTAAGCAGCTTTAAGAAGAAC 226
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QY 592 TGAACCTGATGATTGAGATGATGAGAGCAGACTTTGTTAAGCAGCTTTAAGAAGAAC 651
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|
|
Db 225 TGAACCTGATGATTGAGATGATGAGAGCAGACTTTGTTAAGCAGCTTTAAGAAGAAC 166
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|
|
QY 652 CTCGTTAATGATTGAGAGAGAGAGATGATGAGAGCAGACTTTGTTAAGCAGCTTTAAGAAGAAC 711
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|
|
Db 165 CTCGTTAATGATTGAGAGAGAGAGATGATGAGAGCAGACTTTGTTAAGCAGCTTTAAGAAGAAC 106
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|
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QY 712 ATTGCTGAAGTCTCTCGCATGTTTACCGAATGTTACCGAATCACTGGCCCTTCCAGAGGCTAAGAAAT 771
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|
|
Db 105 ATTGCTGAAGTCTCTCGCATGTTTACCGAATGTTTACCGAATCACTGGCCCTTCCAGAGGCTAAGAAAT 46
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|
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QY 772 TTCTGTTAGTAAAGATGTTCTTTTC 798
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|
Db 45 TTCTGTTAGTAAAGATGTTCTTTTC 19
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RESULT 7
BE893633
LOCUS
DEFINITION 60143643F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3921607 5',
mRNA sequence.
ACCESSION BE893633
VERSION BE893633.1 GI:10355190
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE NIH-MGC http://mgi.nci.nih.gov/
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
TITLE Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
JOURNAL 1 (bases 1 to 963)
COMMENT National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: ATCC/DCTD/DTF
CDNA Library Prepared by: The I.M.A.G.E. Consortium, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM9754 row: n column: 08
High quality sequence stop: 707.
Location/Qualifiers
1..963
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3921607"
/tissue_type="melanotic melanoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_72"
/note="Organ: skin; Vector: pCMV-Sport6; Site: 1: NotI;
Site: 2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 2 Kb. Library constructed by Life
Technologies."

FEATURES
SOURCE
1..963
Query Match 78.4%; Score 627.4; DB 10; Length 963;
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Best Local Similarity 92.6%; Pred. No. 1.3e-159;
Matches 705; Conservative 0; Mismatches 46; Indels 10; Gaps 4;
QY 42 ACCGATAAAAACAGAGAGAGTGGCTGTAGATCCTGAAACTGTGTTTAAACCTGCCAGGAA 101
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|
|
Db 1 ACCGATAAAAACAGAGAGAGTGGCTGTAGATCCTGAAACTGTGTTTAAACCTGCCAGGAA 60
|
|
|
QY 102 TGTGACAGTCTTCTGATATCAGAAAGGAGAGGATGCGCTTGTGGCAAGGAAACAGGAA 161
|
|
|
Db 61 TGTGACAGTCTTCTGATATCAGAAAGGAGAGGATGCGCTTGTGGCAAGGAAACAGGAA 120
|
|
|
QY 162 GCAGGAGACAGCCTTATTGCAAGGCTCTGCCATGTCCTGCAAGGAAAGAGAGCTTTATCAGGAA 221
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|
|
Db 121 GCAGGAGACAGCCTTATTGCAAGGCTCTGCCATGTCCTGCAAGGAAAGAGAGCTTTATCAGGAA 180
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|
|
QY 222 CATGCTATTCCACCGAGCAATTCGATCTTCAGATTCAGATTCAGATTCAGATTCAGATTCAGATTC 281
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|
|
Db 181 CATGCTATTCCACCGAGCAATTCGATCTTCAGATTCAGATTCAGATTCAGATTCAGATTCAGATTC 240
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|
|
QY 282 GATAGGATGATGCAAGAAACCTGGTAGCAATGCACTGTGGAGGAGAAACGTTTACCAGCAGT 341
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|
Db 241 GATAGGATGATGCAAGAAACCTGGTAGCAATGCACTGTGGAGGAGAAACGTTTACCAGCAGT 300
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QY 342 TTCTCTGGAGATGACCTAGAAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 401
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Db 301 TTCTCTGGAGATGACCTAGAAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 360
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|
|
QY 402 ATTAATGCTGATATATAAAACGTTAAATTTAGTGAAGGAACTCCGATGCGTTGGACAAAATAT 461
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|
|
Db 361 ATTAATGCTGATATATAAAACGTTAAATTTAGTGAAGGAACTCCGATGCGTTGGACAAAATAT 420
|
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|
QY 462 GAAAAATCTTCGAAATGCTTTGAAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 521
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|
|
Db 421 GAAAAATCTTCGAAATGCTTTGAAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 480
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|
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QY 522 TTTGAATCCATCATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 581
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|
|
Db 481 TTTGAATCCATCATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540
|
|
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QY 582 AAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 641
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|
Db 541 AAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 599
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|
QY 642 AATGATATATCTGTTAATGATTTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 698
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|
Db 600 AATGATATATCTGTTAATGATTTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 659
|
|
|
QY 699 AATG---GAGCAGGATATGCTGAAGTCTCTGCGATATGTTACCGAATCAATAGAGCTT 755
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|
Db 660 AATGGAGCAGCAGCATAATTTGCTGAAGTCTCTGCGATATGTTACCGAATCAATAGAGCTT 716
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QY 756 CCAGAGGCTTAAAGAAATTTCTGTTAGTAAAGAGATGTTCTTTT 796
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Db 717 CCAGAGGTTAAAGAAATTTCTGTTAGTAAAGAGATGTTCTTTT 757
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|
|

RESULT 8
BQ020473
LOCUS
DEFINITION BQ020473 690 bp mRNA linear EST 17-JUN-2002
IMAGE:5877002 3', mRNA sequence.
ACCESSION BQ020473
VERSION BQ020473.1 GI:19755751
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 690)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
JOURNAL
```

COMMENT

Contact: Robert Strausberg, Ph.D.
 Email: c9apbs-remail.nih.gov
 Tissue Procurement: Dr. Mary Hendrix
 cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
 cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
 Clone Distribution: Clone distribution information can be found
 through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
 Seq primer: M13 FORWARD
 POLYA=Yes.

FEATURES

source

Location/Qualifiers

1. .690

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:5877002"

/tissue_type="Fibrosarcoma"

/lab_host="DH10B (Life Technologies)"

/clone_lib="NCI CGAP Fsl"

/note="Vector: pT73-Pac (Pharmacia) with a modified
 polylinker; Site 1: EcoR I; Site 2: Not I; NCI CGAP Fsl is
 a cDNA library containing the following tissue(s):
 Fibrosarcoma Cell line HT-1080 (ATCC number CCL-121). The
 library was constructed according to Bonaldo, Lennon and
 Soares, Genome Research, 6:791-806, 1996. First strand
 cDNA synthesis was primed with an oligo-dT primer
 containing a Not I site. Double stranded cDNA was ligated
 to an EcoR I adaptor, digested with Not I, and cloned
 directionally into pT73-Pac vector. The oligonucleotide
 used to prime the synthesis of first-strand cDNA contains
 a library tag sequence that is located between the Not I
 site and the (dT)18 tail. The sequence tag for this
 library is GTTCTACGAG.
 TAG_TISSUE=fibrosarcoma
 TAG_LIB=UI-H-DPO
 TAG_SEQ=GTTCTACGAG"

ORIGIN

Query Match 78.0%; Score 623.9; DB 12; Length 690;

Best Local Similarity 97.4%; Pred. No. 1.2e-158;

Matches 634; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

QY 150 AGGAAACAGGAGCAGGACGCTTATTGAGGCTCTGCCATGTCCTCAAGAAAGAGG 209

DB 690 AGGAAACAGGAGCAGGACGCTTATTGAGGCTCTGCCATGTCCTCAAGAAAGAGG 631

QY 210 CTTATCAGCAGCATCTATTCACCCAGCAATGGATTCTCAGATTGATGACTTCACT 269

DB 630 CTTATCAGCAGCATCTATTCACCCAGCAATGGATTCTCAGATTGATGACTTCACT 571

QY 270 GGTTCAGCAAGATAGGATGATGCAAGAACCTGTTAGCAATGCCCTGTGGGGAAC 329

DB 570 GGTTCAGCAAGATAGGATGATGCAAGAACCTGTTAGCAATGCCCTGTGGGGAAT 511

QY 330 GTTACCAGCAGTTTCTCTGGAGATGACCTAGAAATGCAAGAAACAGCCCTCTCTCCCAA 389

DB 510 GTTACCAGCAATTTCTCTGGAGATGACCTAGAAATGCAAGAAACAGCCCTCTCTCCCAA 451

QY 390 AGCCACGCAAAATTAATCTGTATATAAAGCTTAATAGTGAAGAACTCCGATCGCTT 449

DB 450 AGCCACGCAAAATTAATCTGTATATAAAGCTTAATAGTGAAGAACTCCGATCGCTT 391

QY 450 GGACAAAATATGAAAAATCTTCGAAATGCTTTGAGGAGTGCAGGACCTACTGCAGTC 509

DB 390 GGACAAAATATGAAAAATCTTCGAAATGCTTTGAGGAGTGCAGGACCTACTGCAGTC 331

QY 510 AGGAACGATTTTGAATCCATCATCAGGAGCAGCAGATGATGATGAGCAGACTTT 569

DB 330 AGGAACGATTTTGAATCCATCATCAGGAGCAGCAGATGATGATGAGCAGACTTT 271

QY 570 GTTAAGCACCCTTAAGAGAACTGAAACCTGATGATTGAGAACTTTGTCCTCGAGGAT 629

DB 270 GTTAAGCACCCTTAAGAGAACTGAAACCTGATGATTGAGAACTTTGTCCTCGAGGAT 211

QY 630 TATCACACCCCAATGCATTAATCTCGTTAATGATTCAGGAGAGAAAGGATCAGATTGCT 689
 DB 210 TATCACACCTCAATGCATTAATCTCGTTAATGATTCAGGAGAGAAAGGATCAGATTGCT 151
 QY 690 GTTTTCTTACAATGGAGCAGGATATTCCTGAAGTCTCTCTGGCATATGTTACCGAATCAAT 749
 DB 150 GTTTTCTTACAATGGAGCAGGATATTCCTGAAGTCTCTCTGGCATATGTTACCGAATCAAT 91
 QY 750 AGCTTCCAGAGCTAAGAAATTTCTGTAGTAAAGATGTTCTTTTCCC 800
 DB 90 GGCCTTCCAGAGCTAAGAAATTTCTGTAGTAAAGATGTTCTTTTCCC 40

RESULT 9

BI460396

LOCUS

DEFINITION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Contact: Robert Strausberg, Ph.D.

Email: c9apbs-remail.nih.gov

Tissue Procurement: Miklos Falkovits, M.D., Ph.D.

cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki

Toshiyuki and Piero Carninci (RIKEN)

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

Plate: LLAM11675 row: f column: 17

High quality sequence stop: 643.

FEATURES

source

1. .653

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:5267728"

/lab_host="DH10B"

/clone_lib="NIH MGC 97"

/notes="Organ: testis; Vector: pBluescriptR (modified

pBluescript KS+); Site 1: BamHI; Site 2: SalI-XhoI

(gtcgag); Oligo-dT primed using primer

5'-TTTTTTTTTTTTTTVN-3', size-selected for average

insert size 2.2 kb and normalized to 10⁶. This is a

primary library enriched for full-length clones and

constructed using the Cap-trapper method (Carninci, in

preparation). Library constructed by M. Brownstein

(NIH/NHGRI, National Institutes of Health). Note: this is

a NIH_MGC Library."

ORIGIN

Query Match 76.6%; Score 613; DB 12; Length 653;

Best Local Similarity 99.8%; Pred. No. 1e-155;

Matches 624; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 CTCTCTCCAGCAGGTCAGGACTTCAGGACTCAAAATGACCGATAAACAAGAGG 60

DB 29 CTCTCTCCAGCAGGTCAGGACTTCAGGACTCAAAATGACCGATAAACAAGAGG 88

QY 61 TGGCTGTAGATCTCTGAAACTGTGTTTAAACGTCCAGGGAAATGTGACAGTCCTTCGATC 120

DB 89 TGGCTGTAGATCTCTGAAACTGTGTTTAAACGTCCAGGGAAATGTGACAGTCCTTCGATC 148


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/lab_host="DH10B (Life Technologies)"
/clone_lib="NCI CGAP DT1"
/notes="Organ: Lung; Vector: p7773-Pac (Pharmacia) with a
modified polylinker; Site_1: Ecor I; Site_2: Not I;
NCI CGAP DT1 is a normalized cDNA library containing the
following tissue(s): Metastatic Chondrosarcoma in Lung.
The library was constructed according to Bonaldo, Lennon
and Soares, Genome Research, 6:791-806, 1996. First strand
cDNA synthesis was primed with an oligo-dT primer
containing a Not I site. Double stranded cDNA was ligated
to an Ecor I adaptor, digested with Not I, and cloned
directionally into p7773-Pac vector. The oligonucleotide
used to prime the synthesis of first-strand cDNA contains
a library tag sequence that is located between the Not I
site and the (dT)18 tail. The sequence tag for this
library is AACTGTTCCG.
TAG TISSUE=lung metastatic chondrosarcoma
TAG_LIB=UI-H-DT1
TAG_SEQ=AACTGTTCCG"

ORIGIN
Query Match      76.5%; Score 611.8; DB 12; Length 660;
Best Local Similarity 99.5%; Pred. No. 2.1e-155;
Matches 624; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

QY 174 CTTATTGCAGGCTCTGCCATGTCCTCAAGAGAAAGAGCTTATGACAGGACATGCTATTCCA 233
Db 660 CTTATTGCAGGCTCTGCCATGTCCTCAAGAGAAAGAGCTTATGACAGGACATGCTATTCCA 601
QY 234 CCCAGCCAAATGGGATTTCTCAGATTGATGACTTCACTGGTTTCAGCAAGATAGGATGATG 293
Db 600 CCCAGCCAAATGGGATTTCTCAGATTGATGACTTCACTGGTTTCAGCAAGATAGGATGATG 541
QY 294 CAGAAACCTGTAGCAATGACACCTGTGGAGGAAAGCTTACCGAGCTTCTCTGGAGAT 353
Db 540 CAGAAACCTGTAGCAATGACACCTGTGGAGGAAAGCTTACCGAGCTTCTCTGGAGAT 481
QY 354 GACCTAGAAATGCAGAGAAACAGCCTCTCTCCAAAAGCCAAACGAGAAATTAATGCTGAT 413
Db 480 GACCTAGAAATGCAGAGAAACAGCCTCTCTCCAAAAGCCAAACGAGAAATTAATGCTGAT 421
QY 414 ATAAACCTAAATAGTGAAGAACTCCGATGCGTTGGACAAAATATGAAAAATCTTC 473
Db 420 ATAAACCTAAATAGTGAAGAACTCCGATGCGTTGGACAAAATATGAAAAATCTTC 361
QY 474 GAAATGCTTGAAGAGTGCAGAGGACCTACTGCGTTCAGAGAGCGATTTTGAATCCATC 533
Db 360 GAAATGCTTGAAGAGTGCAGAGGACCTACTGCGTTCAGAGAGCGATTTTGAATCCATC 301
QY 534 ATCAAGGAGCAGCAAGATGATGAGAGAGCTTTGTTAAGACCTTTAAGAGAACTG 593
Db 300 ATCAAGGAGCAGCAAGATGATGAGAGAGCTTTGTTAAGACCTTTAAGAGAACTG 241
QY 594 AAACCTGATGTTGAGATATCTTGTCCCTGGAGGATATACACCCCAAAATGCATAATCT 653
Db 240 AAACCTGATGTTGAGATATCTTGTCCCTGGAGGATATACACCCCAAAATGCATAATCT 181
QY 654 CTTAATGATGAGAGAGAAAGATCAGATGCTGTTTCTTACATGGAGCAGGATAT 713
Db 180 CTTAATGATGAGAGAGAAAGATCAGATGCTGTTTCTTACATGGAGCAGGATAT 121
QY 714 TCGTGAAGTCTCCTGCGATATGTTACCGAATCAATAGCCTTCCAGAGGCTTAAGAAATTT 773
Db 120 TCGTGAAGTCTCCTGCGATATGTTACCGAATCAATAGCCTTCCAGAGGCTTAAGAAATTT 62

774 CTGTTAGTAAAGATGTTCTTTTCCC 800
61 CTGTTAGTAAAGATGTTCTTTTCCC 35

RESULT 11
BM761296 642 bp mRNA linear EST 04-MAR-2002
LOCUS
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121 AGAAAAGGCGAGAGATGGCCCTTTGGCAAGGAAAACAGAGAGCAGAGACACCTTTATG 180
149 AGAAAAGGCGAGAGATGGCCCTTTGGCAAGGAAAACAGAGAGCAGAGACACCTTTATG 208
181 CAGGCTCTGCGATGTCCTCAAGAGAAAGAGCTTATGACAGGACATGCTATTCACCCAGCC 240
209 CAGGCTCTGCGATGTCCTCAAGAGAAAGAGCTTATGACAGGACATGCTATTCACCCAGCC 268
241 AATTGATTTCTCAGATTGATGATCTCACTGGTTTCAGCAAGATAGGATGATGCAAGAAC 300
269 AATTGATTTCTCAGATTGATGATCTCACTGGTTTCAGCAAGATAGGATGATGCAAGAAC 328
301 CTGTAGCAATGACCTGTGGAGGAAAGCTTACCGAGCTTCTCTGGAGATGACCTAG 360
329 CTGTAGCAATGACCTGTGGAGGAAAGCTTACCGAGCTTCTCTGGAGATGACCTAG 388
361 AATGACAGAGAAACAGCCTCTCTCCAAAAGCCAAACGAGAAATTAATGCTGATATAAAC 420
389 AATGACAGAGAAACAGCCTCTCTCCAAAAGCCAAACGAGAAATTAATGCTGATATAAAC 448
421 GTAATTTAGTGAAGAACTCCGATGCTGACAAAATATGAAAAATCTTCGAAATGC 480
449 GTAATTTAGTGAAGAACTCCGATGCTGACAAAATATGAAAAATCTTCGAAATGC 508
481 TTGAAGGAGTGCAGGACCTACTGCACTCAGGAGCGATTTTGTGAATCCATCATCAAGG 540
509 TTGAAGGAGTGCAGGACCTACTGCACTCAGGAGCGATTTTGTGAATCCATCATCAAGG 568
541 AAGCAGCAAGATGATGAGAGGACCTTGTGAAGCACCCTTAAGAGAACTGAAACGTA 600
569 AAGCAGCAAGATGATGAGAGGACCTTGTGAAGCACCCTTAAGAGAACTGAAACGTA 628
601 TGATTT-GAGAAATCTTGTCCCTGG 624
629 TGATTTGAGAAATCTTGTCCCTGG 653

RESULT 10
BM998183/3
LOCUS
DEFINITION
UI-H-DT1-awc-o-07-0-UI.s1 NCI CGAP DT1 Homo sapiens cDNA clone
IMAGE:5887710 3', mRNA sequence.
ACCESSION
BM998183
VERSION
BM998183.1 GI:19723084
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 660)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Dr. Jose Mercuende
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
DNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Seq primer: M13 FORWARD
POLYA=Yes.
Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5887710"
/tissue type="Metastatic Chondrosarcoma"
/dev_stage="Adult"
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DEFINITION K-EST0042057 S13KMS5 Homo sapiens cDNA clone S13KMS5-2-E10 5', mRNA
sequence.
ACCESSION BM761296
VERSION BM761296.1 GI:19090897
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 642)
AUTHORS Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
Kim,Y.S.
TITLE 21C Frontier Korean EST Project 2001
JOURNAL Unpublished (2002)
COMMENT Contact: Kim YS
Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Boeun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
Email: yongsung@mail.kribb.re.kr
Plate: 2 row: E column: 10
High quality sequence stop: 642.
FEATURES
Location/Qualifiers
1..642
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="S13KMS5-2-E10"
/tissue_type="myeloma"
/cell_line="KMS-5"
/lab_host="Top10p/"
/clone_lib="S13KMS5"
(note="Vector: PCMS; Site 1: EcoRI; Site 2: NotI; The poly
(A)+ RNA was dephosphorylated with bacterial alkaline
phosphatase (BAP) and then decapped with tobacco acid
pyrophosphatase (TAP). The decapped intact mRNA was
ligated with DNA-RNA linker including EcoRI site by
treatment of T4 RNA ligase and the first strand cDNA was
synthesized from oligo dt-selected mRNA by priming with
dT-tailed vector. The dt-tailed vector was adjusted to
have about 60nt. The cDNA vector was circularized with E.
coli DNA ligase after digestion of EcoRI which site is
also included in vector. An RNA strand converted to a DNA
strand by Okayama-Berg method. The obtained cDNA vectors
were used for transformation of competent cells E. coli
Top10p' by electroporation method. The cDNA libraries
constructed by this method are full-length enriched cDNA
library."
ORIGIN
Query Match 76.4%; Score 611.2; DB 12; Length 642;
Best Local Similarity 98.7%; Pred. No. 3.1e-155;
Matches 616; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
QY 16 GTCAGACTTCAGGACTGAAACCAATGACCGATTAACACAGAGAGGCTGGCTGTAGATCTGT 75
DB 19 GTCTCTCTCCACGACAGGAAACAATACCGATTAACACAGAGAGGCTGGCTGTAGATCTGT 78
QY 76 AAACCTGTGTTTAAACGCTCCACGGAATGTGACAGTCTCTTCGTATCAGAAAGCGCAGAGGA 135
DB 79 AAACCTGTGTTTAAACGCTCCACGGAATGTGACAGTCTCTTCGTATCAGAAAGCGCAGAGGA 138
QY 136 TGGCCCTGTGTGGCAAGAAACAAGGACGAGGACGCTTATTCAGGCTCTGCCATGT 195
DB 139 TGGCCCTGTGTGGCAAGAAACAAGGACGAGGACGCTTATTCAGGCTCTGCCATGT 198
QY 196 CCAAGAAAGAAAGCTTATGACAGGACATGCTATTCCACCCAGCAATTTGGATTCTTCAGA 255
DB 199 CCAAGAAAGAAAGCTTATGACAGGACATGCTATTCCACCCAGCAATTTGGATTCTTCAGA 258
QY 256 TTGATGACTTCTACTGTTTTCAGCAAGATAGATGATGTCAGAAACCTGTAGCAATGCAC 315

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DB 259 TTGATGACTTCTACTGTTTTCAGCAAGATAGATGATGTCAGAAACCTGTAGCAATGCAC 318
QY 316 CTGTGGAGGAAACGTTACCAAGCTTCTCTGGAGATGACCTAGATGTCAGAGAAACAG 375
DB 319 CTGTGGAGGAAACGTTACCAAGCTTCTCTGGAGATGACCTAGATGTCAGAGAAACAG 378
QY 376 CTTCTCTCTCCCAAGCCCAACGAGAAATTAATGCTGATATAAAAGCTAAATTAGTGAAGG 435
DB 379 CTTCTCTCTCCCAAGCCCAACGAGAAATTAATGCTGATATAAAAGCTAAATTAGTGAAGG 438
QY 436 AACTCCGATGCGTTGACACAAAATATGAAAAAATCTTGGAAATGCTTGAAGGAGTGCAAG 495
DB 439 AACTCCGATGCGTTGACACAAAATATGAAAAAATCTTGGAAATGCTTGAAGGAGTGCAAG 498
QY 496 GACCTACTGAGTCAGAGGAGGATTTTGAATCCATCATCAGGAGGACAGCAAGATGTA 555
DB 499 GACCTACTGAGTCAGAGGAGGATTTTGAATCCATCATCAGGAGGACAGCAAGATGTA 558
QY 556 TGAGACGAGACTTTGTTAAGCACCTTTAAGCAAACTTAAGCAAACTGAACGATGATTTGAGATACT 615
DB 559 TGAGACGAGACTTTGTTAAGCACCTTTAAGCAAACTTAAGCAAACTGAACGATGATTTGAGATACT 618
QY 616 TGTCCCTGGAGGATTTATCACACC 639
DB 619 TGTCCCTGGAGGATTTATCACACC 642

RESULT 12
LOCUS AV700754 696 bp mRNA linear EST 16-JAN-2002
DEFINITION AV700754 GKC Homo sapiens cDNA clone GKCRA02 3', mRNA sequence.
ACCESSION AV700754
VERSION AV700754.1 GI:10302725
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 696)
AUTHORS Xu,X., Huang,J., Xu,Z., Qian,B., Zhu,Z., Yan,Q., Cai,T., Zhang,X.,
Xiao,H., Qu,J., Liu,F., Huang,Q., Cheng,Z., Li,N., Du,J., Hu,W.,
Shen,K., Lu,G., Fu,G., Zhong,M., Xu,S., Gu,W., Huang,W., Zhao,X.,
Hu,G., Gu,J., Chen,Z. and Han,Z.
TITLE Insight into hepatocellular carcinogenesis at transcriptome level
by comparing gene expression profiles of hepatocellular carcinoma
with those of corresponding noncancerous liver
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 98 (26), 15089-15094 (2001)
MEDLINE 21625106
PUBMED 11752456
COMMENT Contact: Zeguang Han
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
Tel: 86-21-50801919 (ex.45)
Fax: 86-21-50801922
Email: hanzg@chgc.sh.cn
This clone is available at CHGC in Shanghai.
FEATURES
Location/Qualifiers
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="GKCRA02"
/tissue_type="hepatocellular carcinoma"
/dev_stage="Adult"
/lab_host="SOLR"
/clone_lib="GKC"
notes="vector: pBluescript sk(-); Site_1: EcoRI; Site_2:
XhoI"
ORIGIN
Query Match 75.7%; Score 605.4; DB 9; Length 696;

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Best Local Similarity 97.4%; Pred. No. 1.2e-153;
Matches 667; Conservative 0; Mismatches 13; Indels 5; Gaps 5;
QY 120 CAGAAAGGAGAGGAT-GGCCCTGTTGGCAAGAAACAAGAGCA-GGAGACAGCTTA 177
Db 695 CAGAAAGGAGAGGATGGGCTTGTGGCAAGNACCAAGAGGAGGAGGAGGCTTA 636
QY 178 TTGAGGCTCTGCATGTCACAAAGAAAGAGCTTATGACAGGACATGCTATPCCACC- 236
Db 635 TGCAAGGCTCTGCATGTCACAAAC-AAAGAGCTTATGACAGGACATGCTATPCCACC 577
QY 237 AGCAATGTGATTCAGATGATGATTC-ACGTGTTTCCAGAAAGATAGGATGATGA 295
Db 576 AGCAATGTGATTCAGATGATGATTC-ACGTGTTTCCAGAAAGATAGGATGATGA 517
QY 296 GAAACCTGTAGCAATCCACTGTGGAGGAAAGCTTACCAGAGATTTCTCTGGAGTGA 355
Db 516 GAAACCTGTAGCAATCCACTGTGGAGGAAAGCTTACCAGAGATTTCTCTGGAGTGA 457
QY 356 CTTAGATGACAGAAACAGCCTCTCTCCAAAGCAACGAGAAATTAATGCTGATAT 415
Db 456 CTTAGATGACAGAAACAGCCTCTCTCCAAAGCAACGAGAAATTAATGCTGATAT 397
QY 416 AAAACGTAATTAAGTGAAGAACTCCGATCGTTGGACAAAATATGAAAAATCTTGA 475
Db 396 AAAACGTAATTAAGTGAAGAACTCCGATCGTTGGACAAAATATGAAAAATCTTGA 337
QY 476 AATCCTTGAAGAGTCAAGACCTACTGACGACAGAAAGCGATTTTGAATCCATAT 535
Db 336 AATCCTTGAAGAGTCAAGACCTACTGACGACAGAAAGCGATTTTGAATCCATAT 277
QY 536 CAAGGAGCAGCAGATGATGACAGCAGACTTGTAAACCTTAAAGAAAGAACTGAA 595
Db 276 CAAGGAGCAGCAGATGATGACAGCAGACTTGTAAACCTTAAAGAAAGAACTGAA 217
QY 596 ACGTATGATGAAATACCTGTCCTGGAGGATTAACACCCCAAAATGCAATPCTCG 655
Db 216 ACGTATGATGAAATACCTGTCCTGGAGGATTAACACCCCAAAATGCAATPCTCG 157
QY 656 TTAATGATGAGGAGAGAAAGATGATGCTGTTTCTCAATGAGGACGATATG 715
Db 156 TTAATGATGAGGAGAGAAAGATGATGCTGTTTCTCAATGAGGACGATATG 97
QY 716 CTGAAGTCTCTGATATGTTACCGAATCAATAGCCTTCCAGAGCTAAGAAATTTCT 775
Db 96 CTGAAGTCTCTGATATGTTACCGAATCAATAGCCTTCCAGAGCTAAGAAATTTCT 37
QY 776 GTTAGTAAAGATGTTCTTTTCCC 800
Db 36 GTTAGTAAAGATGTTCTTTTCCC 12

RESULT 13
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LOCUS AGENCOURT 10580391 NIH_MGC_128 Homo sapiens cDNA clone
DEFINITION IMAGE:6710386 5', mRNA sequence.
ACCESSION BU940543
VERSION BU940543.1 GI:24129362
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 832)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: csapbs-remail.nih.gov
Tissue Procurement: NCI
CDNA Library Preparation: Michael Brownstein Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
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DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LICM3015 row: m column: 10
High quality sequence stop: 465.
Location/Qualifiers
source
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/clone="IMAGE:6710386"
/tissue_type="mixed (pool of 40 RNAs)"
/lab_host="DH10B.(T1-phage-resistant)"
/clone_lib="NIH_MGC_128"
/notes="Vector: pDNR-LIB; Site 1: SfiI (ggccattatggcc);
Site 2: SfiI (ggcgctcgcc); Double-stranded cDNA was
prepared from a pool of 40 cell line polyA+ RNAs (bladder
- 2%, blood - 33.4%, brain - 5.6%, breast - 12.5%, colon -
4%, connective tissue - 1.4%, eye - 1%, intestine - 2.6%,
kidney - 2.2%, liver - 5.7%, lung - 10.8%, NK-cell -
5.2%, ovary - 4%, pharynx - 2.5%, prostate - 4.3%,
salivary gland - 1.3%, and skin - 2.3%). 5' and 3'
adaptors were used in cloning as follows:
5'-AAGCAGTGTATCAACGACAGTGGCCATACGCGCGG-3' and
5'-ATTCTAGAGCGCGGCGGCGACATG-dt(30)NN-3'. Full-length
creator SMART kit and size-selected using the Clontech
size fraction (other fractions present in NIH_MGC_126 and
NIH_MGC_127). Library created in the laboratory of T.
Usdin, M.D., Ph.D. (NIMH, NIH). Note: this is a NIH_MGC
Library."
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ORIGIN

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Query Match 75.0%; Score 599.6; DB 13; Length 832;
Best Local Similarity 95.9%; Pred. No. 4.6e-152;
Matches 637; Conservative 0; Mismatches 24; Indels 3; Gaps 2;
QY 16 GTCAGGACTTCAGACACTGAAACAATACCGATAAAACAGAGAGGCTGTAGATCTG 75
Db 28 GTCTCTCTCCAGCAGGAACAATGACCGATAAAACAGAGAGGCTGTAGATCTG 87
QY 76 AAATGTGTTTAAACGTCCAGGGAATGTGACGTCTTCTGATCAGAAAGGAGAGGA 135
Db 88 AAATGTGTTTAAACGTCCAGGGAATGTGACGTCTTCTGATCAGAAAGGAGAGGA 147
QY 136 TGGCCCTGTTGGCAGGAAACAAGCAGCAGACAGCTTATTGCAAGGCTCTCCCATGT 195
Db 148 TGGCCCTGTTGGCAGGAAACAAGCAGCAGACAGCTTATTGCAAGGCTCTCCCATGT 207
QY 196 CCAAGAAAGAGCTTATGACAGGACATGCTATTCCACCAGCAATTGGATTCTCAGA 255
Db 208 CCAAGAAAGAGCTTATGACAGGACATGCTATTCCACCAGCAATTGGATTCTCAGA 267
QY 256 TTGATGACTTCACCTGTTTCCAGCAAGATAGGATGATGCAAAACCTGGTAGCAATGCAC 315
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QY 376 CCTCTCTCTCCAAAGCCACGAGAAATTAATGCTGATATAAAACGTAATTAAGTAGAGG 435
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QY 436 AACTCCGATGCTTGGACAAAATATGAAAAATCTTCGAAATCTTTGAAAGAGTGAAG 495
Db 448 AACTCCGATGCTTGGACAAAATATGAAAAATCTTCGAAATCTTTGAAAGAGTGAAG 507
QY 496 GACCTACTGCGAGTCAAGAGCGATTTTGTGATCCATCATCAGGAGCAGCAGAGTGA 555
Db 508 GACCTACTGCGAGTCAAGAGCGATTTTGTGATCCATCATCAGGAGCAGCAGAGTGA 567
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QY 556 TGAGACGAGACTTTGTTAAGCACC-TTAAAGAGAAACTGAACCGTATGATTTGAGATAC 614
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Db 568 TGAGACGAGACTTTGTTAAGCACC-TTAAAGAGAAACTGAACCGTATGATTTGAGATAC 627
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QY 615 TTGT--CCCTGGAGGATTAATCAACCCCAAAATGCATATCTCGTTAATGATTTGAGGAG 672
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Db 628 TTGTCCCGGAGGATTAATCAACCCCAAAATGCATATCTCGTTAATGATTTGAGGAG 687
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QY 673 AAAA 676
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Db 688 AAAA 691
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RESULT 14
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LOCUS
DEFINITION
603193727F1 NIH_MGC_95 Homo sapiens cDNA clone IMAGE:5265006 5',
mRNA sequence.
ACCESSION
BI552760
VERSION
BI552760.1 GI:15440072
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 946)
NIH-MGC http://mgi.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
Toshiyuki and Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11668 row: e column: 07
High quality sequence stop: 863.
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/note="Organ: brain; Vector: pBluescriptR (modified
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(gtccag); Oligo-dT primed using primer
5'-TTTTTTTTTTTTTTVN-3', size-selected for average
insert size 2.5 kb and normalized to 10^5. This is a
primary library enriched for full-length clones and
constructed using the Cap-trapper method (Carninci, in
preparation). Library constructed by M. Brownstein
(NIH/NHGRI, National Institutes of Health). Note: this
is a NIH_MGC Library."
ORIGIN
Query Match 73.4%; Score 587.2; DB 12; Length 946;
Best Local Similarity 92.8%; Pred. No. 1.1e-148;
Matches 661; Conservative 0; Mismatches 43; Indels 8; Gaps 4;
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QY 76 AAACCTGTGTTAAACCTCCAGGATGTGACAGTCTTCGTATCAGAAAGGCAGAGA 135
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Db 288 AAACCTGTGTTAAACCTCCAGGATGTGACAGTCTTCGTATCAGAAAGGCAGAGA 347
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Db 348 TGGCCCTGTTGGCAAGGAAACAAGGACGAGGACAGCCCTTATTGCAAGGCTCTGCCATGT 407
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QY 196 CCAAGAAAAGAGAGCTTATGACAGGACATCTCTATTCACCCAGCCCAATTGGATTCTCAGA 255
Db 408 CCAAGCAAAAGAGCTTATGACAGGACATCTCTATTCACCCAGCCCAATTGGATTCTCAGA 467
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QY 256 TTGATGACTTTCACTGGTTTCAGCAAGATAGGATGATGAGAAACCTGGTAGCAATGCAC 315
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QY 316 CTGTGGAGGAAAGCTTTACAGCAGAGTTTCTCTGGAGATGACCTAGATGACAGAGAAACAG 375
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QY 436 AACTCCGATCGTTGGACAAAATAATGAAAAATCTTCGAAATGCTTTGAAAGGATGCAAG 495
Db 648 AACTCCGATCGTTGGACAAAATAATGAAAAATCTTCGAAATGCTTTGAAAGGATGCAAG 707
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QY 496 GACCTACTCGAGTCAGGAGCGATTTTTCGAAATCCATCATCAAGGAGCAGCAGAGATGTA 555
Db 708 GACCTACTCGAGTCAGGAGCGATTTTTCGAAATCCATCATCAAGGAGCAGCAGAGATGTA 767
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QY 556 TGAGACGAGA---CTTTGTTAAGCACCTTAAGAAAGAAACTGAAACCGTAT-GATTGAGAA 611
Db 768 ATGAGACGAGAGACCTTTGTTAAGCACCTTAAGAAAGAAACTGAAACCGTATGATTGAGAA 827
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QY 612 TACTTGTCCCTGGAGGATTAATCAACCCCAAAATGCAATCTCGTTAATGATTGAGG--A 669
Db 828 TTTGTGTCCTGGAGGATTAATCAACCCCAAAATGCAATCTCGTTAATGATTGAGGAG 887
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QY 670 GAGAAAAGGATCAGATTCG--TGTTTTCTACAATGGAGCAGGATATTGCTGA 719
Db 888 CGCACAGGCTCCGATTCGTTGTTCTCAATGGAGCAGAGATATTGCTGA 939
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RESULT 15
CA419457 614 bp mRNA linear EST 07-NOV-2002
LOCUS
DEFINITION
UT-H-FHO-bci-m-22-0-UI.s1 NCI CGAP FHO Homo sapiens cDNA clone
UT-H-FHO-bci-m-22-0-UI 3', mRNA sequence.
ACCESSION
CA419457
VERSION
CA419457.1 GI:24782112
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 614)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
Tissue Procurement: James Martin
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
DNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be obtained
from Dr. M. Bento Soares, bento-soares@uiowa.edu
Seq primer: M13 FORWARD
POLYA=Yes.
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Location/Qualifiers
1..614
/organism="Homo sapiens"
source

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Search completed: April 26, 2004, 01:59:02
Job time : 1457.53 secs

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/dev_stage="Adult"  
/lab_host="DH10B (Life Technologies)"  
/clone_lib="NCI CGAP FHO"  
/notes="Organ: Bone; Vector: pT7T3-Pac (Pharmacia) with a  
modified polylinker; Site 1: EcoR I; Site 2: Not I;  
NCI CGAP FHO is a cDNA library containing the following  
tissue(s): Human Grade 1 Chondrosarcoma Cell Line The  
library was constructed according to Bonaldo, Lennon and  
Soares, Genome Research, 6:791-806, 1996. First strand  
cDNA synthesis was primed with an oligo-dT primer  
containing a Not I site. Double stranded cDNA was ligated  
to an EcoR I adaptor, digested with Not I, and cloned  
directionally into pT7T3-Pac vector. The oligonucleotide  
used to prime the synthesis of first-strand cDNA contains  
a library tag sequence that is located between the Not I  
site and the (dT)18 tail. The sequence tag for this  
library is AGAATCCGGC. The cell line was provided by Dr  
James Martin from University of Iowa  
TAG TISSUE=Human Chondrosarcoma Cell Line CS8 - Grade 1  
Chondrosarcoma  
TAG LIB=UI-H-RHO  
TAG_SEQ=AGAATCCGGC"
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ORIGIN

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Query Match      72.0%; Score 576; DB 14; Length 614;  
Best Local Similarity 99.0%; Pred. No. 1.1e-145;  
Matches 590; Conservative 0; Mismatches 5; Indels 1; Gaps 1;  
  
QY 206 GAAGCTTATCAGAGGACGTCTTCCCA-CCGAGCCAAATGGATCTCAGATTGATGACT 264  
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QY 265 TCACTGGTTTCAGCAAGATAGGATGATGCAGAAACCTGGTAGCAATGCACCTGTGGGAG 324  
Db 554 TCACTGGTTTCAGCAAGATAGGATGATGCAGAAACCTGGTAGCAATGCACCTGTGGGAG 495  
  
QY 325 GAACCTTACACAGCTTTCTCGGAGATGACCTAGAAATGCGAGAGAACAGCCTCTCTC 384  
Db 494 GAACCTTACACAGCTTTCTCGGAGATGACCTAGAAATGCGAGAGAACAGCCTCTCTC 435  
  
QY 385 CCAAAAGCCCAAGAGAAATTAATGCTGATATAAAACGTAATAGTGAAGGAACCTCCGAT 444  
Db 434 CCAAAAGCCCAAGAGAAATTAATGCTGATATAAAACGTAATAGTGAAGGAACCTCCGAT 375  
  
QY 445 GCCTTGGACAAAATATGAAAAATCTTCGAATGCTTGAAGAGTGCAGGACCTACTG 504  
Db 374 GCCTTGGACAAAATATGAAAAATCTTCGAATGCTTGAAGAGTGCAGGACCTACTG 315  
  
QY 505 CAGTCAGGAAGCGATTTTGTGAATCCATCATCAAGGAAGCAGCAAGATGTATGAGACGAG 564  
Db 314 CAGTCAGGAAGCGATTTTGTGAATCCATCATCAAGGAAGCAGCAAGATGTATGAGACGAG 255  
  
QY 565 ACTTTGTTAAGACCTTAAGAGAAACTGAAACGTAATGATTTGAGAAATCTTGTCCCTGG 624  
Db 254 ACTTTGTTAAGACCTTAAGAGAAACTGAAACGTAATGATTTGAGAAATCTTGTCCCTGG 195  
  
QY 625 AGGATTATCACCCCAATGCAATATCTCGTTAATGATTGAGGAGAGAGAAAGGATCAGA 684  
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QY 685 TTGCTGTTTTCTCAATGGAGCAGGATATTGCTGAAGTCTCTCTGGCATATGTTACCGAAT 744  
Db 134 TTGCTGTTTTCTCAATGGAGCAGGATATTGCTGAAGTCTCTCTGGCATATGTTACCGAAT 75  
  
QY 745 CAAATAGCCTTCAGAGGCTTAAGAAATTTCTGTAGTAAAGATGTTCTTTTCCC 800  
Db 74 CAACTGCGCTTCAGAGGCTTAAGAAATTTCTGTAGTAAAGATGTTCTTTTCCC 19
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model
Run on: April 25, 2004, 07:15:18 ; Search time 39.687 Seconds
(without alignments)
1186.557 Million cell updates/sec

Title: US-10-051-835-12
Perfect score: 800
Sequence: 1 cttctccagcaggtcag.....taaaagatgtctttttccc 800

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: /cgn2_6/ptodata/2/ina/5B.COMB.seq:
3: /cgn2_6/ptodata/2/ina/6A.COMB.seq:
4: /cgn2_6/ptodata/2/ina/6B.COMB.seq:
5: /cgn2_6/ptodata/2/ina/PTUS.COMB.seq:
6: /cgn2_6/ptodata/2/ina/backfiles1.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	223.6	27.9	3812	4	US-09-784-316-1
2	70.6	8.8	65042	4	US-09-784-316-3
3	52	6.5	7218	1	US-08-232-463-14
4	37.2	4.7	6008	1	US-07-789-915A-5
5	37.2	4.7	6008	1	US-08-005-002C-5
6	37.2	4.7	6008	1	US-08-487-203A-5
7	36.8	4.6	656	4	US-08-936-165A-87
8	35.8	4.5	4084	3	US-08-866-340-1
9	35.8	4.5	4460	3	US-09-103-875-4
10	34.2	4.3	5829	4	US-08-809-254A-4
11	34.2	4.3	9828	4	US-08-961-527-41
12	34	4.2	981	4	US-09-543-681A-3279
13	32.6	4.1	505	4	US-09-621-976-15639
14	32.6	4.1	87350	3	US-08-781-891-79
15	32.6	4.1	87350	4	US-09-618-166-79
16	32.6	4.1	87543	4	US-09-791-211-3
17	32.4	4.0	561	4	US-09-328-352-3577
18	32	4.0	2718	4	US-09-134-000C-1015
19	31.8	4.0	1329	4	US-09-134-001C-196
20	31.6	4.0	1914	4	US-09-434-681A-1697
21	31.6	4.0	2169	4	US-09-434-408-3
22	31.4	3.9	1101	4	US-09-891-641-67
23	31.4	3.9	2013	4	US-09-543-681A-1807
24	31.4	3.9	4034	4	US-09-883-134-5
25	31.2	3.9	1272	4	US-09-134-001C-2358
26	31	3.9	366	4	US-09-134-001C-997
27	31	3.9	481	4	US-09-621-976-211

C 28	31	3.9	832	4	US-09-621-976-2813	Sequence 2813, Ap
C 29	31	3.9	1237	4	US-09-620-312D-419	Sequence 419, Ap
C 30	31	3.9	1311	4	US-09-833-381-872	Sequence 872, Ap
C 31	31	3.9	3429	4	US-09-936-989A-1	Sequence 1, Appl
C 32	31	3.9	4342	3	US-09-338-907-107	Sequence 107, Ap
C 33	31	3.9	4342	4	US-09-218-207-107	Sequence 107, Ap
C 34	31	3.9	4582	3	US-09-338-907-118	Sequence 118, Ap
C 35	31	3.9	4582	4	US-09-218-207-118	Sequence 118, Ap
C 36	31	3.9	4686	3	US-09-338-907-117	Sequence 117, Ap
C 37	31	3.9	4686	4	US-09-218-207-117	Sequence 117, Ap
C 38	31	3.9	4875	3	US-09-338-907-114	Sequence 114, Ap
C 39	31	3.9	4875	4	US-09-218-207-114	Sequence 114, Ap
C 40	31	3.9	4958	3	US-09-338-907-116	Sequence 116, Ap
C 41	31	3.9	4958	4	US-09-218-207-116	Sequence 116, Ap
C 42	31	3.9	4986	3	US-09-338-907-121	Sequence 121, Ap
C 43	31	3.9	4986	4	US-09-218-207-121	Sequence 121, Ap
C 44	31	3.9	5020	3	US-09-338-907-120	Sequence 120, Ap
C 45	31	3.9	5020	4	US-09-218-207-120	Sequence 120, Ap

ALIGNMENTS

RESULT 1
US-09-784-316-1
; Sequence 1, Application US/09784316
; Patent No. 6461843
; GENERAL INFORMATION:
; APPLICANT: WEI, Ming-Hui et al.
; TITLE OF INVENTION: ISOLATED HUMAN ENZYME PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN ENZYME PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CLO01139
; CURRENT APPLICATION NUMBER: US/09/784,316
; CURRENT FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 3812
; TYPE: DNA
; ORGANISM: Human
US-09-784-316-1

Query Match 27.9%; Score 223.6; DB 4; Length 3812;
Best Local Similarity 64.6%; Pred. No. 6.9e-60;
Matches 384; Conservative 0; Mismatches 174; Indels 36; Gaps 2;

Qy	212	TATGACGAGCATGCTATTTCACCCAGCCCAATGGATTCTCAGATTGATGACTTCACTCG	271
Db	2429	TATGACGAGGATCTTTATGCCACCAACCAAGTGGATTCTCTGTGACGACTTCAAG	2488
Qy	272	TTTCAGCAAGATAGGATGATGACAGAACTGGTAGCAATGCACCTGTGGAGGAAACGT	331
Db	2489	TCTCAGCAAGATGGGCTGATTCAAAACCTGGTAGTACGATTGTAGGAGGACCAA	2548
Qy	332	TACCACAGTTCTCTGGGAGATGACCTAGAAATGCAGAGAAACAGCCTC	379
Db	2549	AAACTGCAGTCTCTCGTAGATGACCAAAAGACCAGTAGCATCTACTTTGGAGCTAT	2608
Qy	380	-----CTCTCCCAAAAGCCCAAGAGAAATTAATGCTGATATAAAGC	421
Db	2609	GCCAAATACATTACAATCACTCTGCTATGSCACAGGAATCAATGCTGATATAAACA	2668
Qy	422	TAAATTAGTGAAGGAATCCGATGGGTGGCAAAAAATATGAAAAAATCTTCAAAATGCT	481
Db	2669	TCAATTAATGAAGGAAGTTTGAAGAGTTTGGTGGAAAAATATGAAGAAATTTTCATTTGCT	2728
Qy	482	TGAAGAGTGCAGGACCTACTGCAGTCAGGAGGAGGATTTTGTGATCCATCATCAAGGA	541
Db	2729	TGAAGAGTGCAGGACCTCTTGAGATGAAGAAACAGTTTGTGATTTACCATCAAGGA	2788
Qy	542	AGCAGCAAGATGTATGAGACGAGACTTTGTTAAGCACCTTAAGAGAAACCTGAACGTAT	601

Db	2789	AGCGCGAAGGGTTAAAGACGAGTCCTAAATTCAGTACCTTTGAGAAGGTA	CTGAGAAAAAT	2848
Qy	602	GATTTGAGAATCTATTGTCCCTGGAGGATTATCACACCCCAAAATGCATAATCTCGTTAAATG		661
Db	2849	AAATTCCCACCACTTCACAAACACATTAGTTCACATCAACAGCAGATCATCATGTTTAGTG		2908
Qy	662	-----ATTGAGGAGAGAAAAAGGATCAGATTGCTGTTTTCTACAAATGGACGACGATATTG		715
Db	2909	CAAAGACCACTGAGAAAAAAATGACAAGTTTTCTGTGCTGTAGATGGAACAGGATATTG		2968
Qy	716	CTGAAGTCTCTGSCATATGTTACCGAATCAATAGCCTCCAGAGCTAAGAA		769
Db	2969	TTCAAGCCTCTCGAATGTTTTGACTCAAGGGAATGTCTTCCAGATGCTAAGAA		3022

```

RESULT 2
US-09-784-316-3
; Sequence 3, Application US/09784316
; Patent No. 6461843
; GENERAL INFORMATION:
; APPLICANT: WEI, Ming-Hui et al.
; TITLE OF INVENTION: ISOLATED HUMAN ENZYME PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN ENZYME PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CLO01139
; CURRENT APPLICATION NUMBER: US/09/784,316
; CURRENT FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 65042
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(65042)
; OTHER INFORMATION: n = A,T,C or G
US-09-784-316-3

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	Query Match	8.8%	Score 70.6;	DB 4;	Length 65042;
	Best Local Similarity	59.6%;	Pred. No. 3.4e-11;		
	Matches 140;	Conservative 0;	Mismatches 89;	Indels 6;	Gaps 1;
Qy	549	AGATGTATGAGACGAGACTTTGTTAAGCACCTTTAAGAGAAACTGAGAACTGATGATGATTTGA	608		
Db	62066	AGSTTTAAAAGACGAGCTCTAAATTCAGTACCTTTGAGAGGTTACTAGAAAAATTAATTC	62125		
Qy	609	GAATACTGTGCCCTGGAGGATTATCACACCCCAATGCATAATCTCGTTTAATGA	662		
Db	62126	CACCACCTTCACAAACAATTAGTGCATCAACAGCAGATCATCATGTTAGTGCAAAGAC	62185		
Qy	663	TTGAGGAGAGAAAAGGATCAGATTGCTGTTTTCTACAA'GGAGCAGGATATTGCTGAAGT	722		
Db	62186	CAGTGAAGAAAAAATGACAAAGTTTCTGTGCTGTAGGATGGACACAGATATTGTTGAAGC	62245		
Qy	723	CTCCTGSCATATGTTACCGAATCAAAATAGCGTTTCCAGAGCGCTAAGAAAAATTTCTGT	777		
Db	62246	CTCTCGAAATGTTTGAGTCAAGGAATGCTGTTTCCAGATGCTTAAGAACGACAGAT	62300		

RESULT 3
US-08-232-463-14/c
; Sequence 14, Application US/08232463
; Patent No. 5670367
; GENERAL INFORMATION:
; APPLICANT: DORNER, F.
; APPLICANT: SCHEIFELINGER, F.
; APPLICANT: FALKNER, F. G.
; TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 1800 Diagonal Road, Suite 500

[illegible]

RESULT 4

US-07-789-915A-5/c
; Sequence 5, Application US/07789915A
; Patent No. 5212058
; GENERAL INFORMATION:
; APPLICANT: Baker, Rohan T.
; APPLICANT: Tobias, John W.
; APPLICANT: Varshavsky, Alexander
; TITLE OF INVENTION: Ubiquitin-Specific Proteases
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02173

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07789,915A
FILING DATE: 19911108
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Brook, David E.
REGISTRATION NUMBER: 22,592
REFERENCE/DOCKET NUMBER: MIT-5091AA
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-861-6240
TELEFAX: 617-861-9540

INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 6008 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: double
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 983..4774
US-07-789-915A-5

Query Match 4.7%; Score 37.2; DB 1; Length 6008;
Best Local Similarity 50.6%; Pred. No. 0.29; Mismatches 0; Gaps 0;
Matches 90; Conservative 0; Indels 88;

QY	565	ACTTTGTTAAGCACCTTAAGAGAACTGAAACGATGATTTGAGAACTGTCCTGGCATATGTTACCGA	742
Db	2413	AAATATTTTCAGGATCCAAAGAGAAAGATTCTGTAGTTTCTGATTATATCTCTATCGGT	2354
QY	625	AGGATTATCACACCCCAATGCAATATCTCGTTAATGATTGAGGAGAGAAAGGATCAGA	684
Db	2353	ATAATAATCGGAACGGAAGATTATAAATGAGTTCTGCTCCAAAGGAGATGAT	2294
QY	685	TTGCTGTTTCTACAATGGAGCAGGATATTGCTGAAGTCTCTCTGGCATATGTTACCGA	742
Db	2293	TTGCTCATTTGGAATTTAATAGAATCCTTGCTCTGGATTCTCCCAATAAATGGAACCAA	2236

RESULT 5

US-08-005-002C-5/c
; Sequence 5, Application US/08005002C
; Patent No. 5494818
; GENERAL INFORMATION:
; APPLICANT: Baker, Rohan T.
; APPLICANT: Tobias, John W.
; APPLICANT: Varshavsky, Alexander
; TITLE OF INVENTION: Ubiquitin-Specific Proteases
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kevin M. Farrell, P.C.

STREET: P.O. Box 999
CITY: York Harbor
STATE: Maine
COUNTRY: U.S.A.
ZIP: 03911

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/005,002C
FILING DATE: 15-JAN-1993
CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/789,915
FILING DATE: 08-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: Farrell, Kevin M.
REGISTRATION NUMBER: 35,505
REFERENCE/DOCKET NUMBER: MIT-5091AAZ
TELECOMMUNICATION INFORMATION:
TELEPHONE: 207-363-0558
TELEFAX: 207-363-0528
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 6008 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 983..4774
US-08-005-002C-5

Query Match 4.7%; Score 37.2; DB 1; Length 6008;
Best Local Similarity 50.6%; Pred. No. 0.29; Mismatches 0; Gaps 0;
Matches 90; Conservative 0; Indels 88;

QY	565	ACTTTGTTAAGCACCTTAAGAGAACTGAAACGATGATTTGAGAACTGTCCTGGCATATGTTACCGA	742
Db	2413	AAATATTTTCAGGATCCAAAGAGAAAGATTCTGTAGTTTCTGATTATATCTCTATCGGT	2354
QY	625	AGGATTATCACACCCCAATGCAATATCTCGTTAATGATTGAGGAGAGAAAGGATCAGA	684
Db	2353	ATAATAATCGGAACGGAAGATTATAAATGAGTTCTGCTCCAAAGGAGATGAT	2294
QY	685	TTGCTGTTTCTACAATGGAGCAGGATATTGCTGAAGTCTCTCTGGCATATGTTACCGA	742
Db	2293	TTGCTCATTTGGAATTTAATAGAATCCTTGCTCTGGATTCTCCCAATAAATGGAACCAA	2236

RESULT 6

US-08-487-203A-5/c
; Sequence 5, Application US/08487203A
; Patent No. 5683904
; GENERAL INFORMATION:
; APPLICANT: Baker, Rohan T.
; APPLICANT: Tobias, John W.
; APPLICANT: Varshavsky, Alexander
; TITLE OF INVENTION: Ubiquitin-Specific Proteases
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kevin M. Farrell, P.C.
; STREET: P.O. Box 999
; CITY: York Harbor
; STATE: Maine
; COUNTRY: U.S.A.
; ZIP: 03911
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,203A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/005,002
FILING DATE: 15-JAN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Farrell, Kevin M.
REGISTRATION NUMBER: 35,505
REFERENCE/DOCKET NUMBER: MIT-5091A32
TELECOMMUNICATION INFORMATION:
TELEPHONE: 207-363-0558
TELEFAX: 207-363-0528
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 6008 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 983..4774
US-08-487-203A-5

Query Match 4.7%; Score 37.2; DB 1; Length 6008;
Best Local Similarity 50.6%; Pred. No. 0.29;
Matches 90; Conservative 0; Mismatches 88; Indels 0; Gaps 0;

QY 565 ACTTTGTTAAGCACTTAAAGAACTGAAAGCTATGATTGAGAACTACTTGTCCCTCG 624
DB 2413 AATATTTTCAGGATCCAAAGAGACAAAGATTCTGATTATATCTATCGGT 2354
QY 625 AGGATTATCACCCCAATGCAATATCTGTTAATGATTGAGAGAGAAAGGATCAGA 684
DB 2353 ATAATAATGCGAAACGGAAGATTAAATAAATGAGGTTCTCGCTCCAAAGGAGAAATGAGT 2294
QY 685 TTGCTGTTTCTACATGAGGAGGAGATATGCTGAAGTCTCCGCGATATGTTACCGA 742
DB 2293 TTGCTCATTTGGAATTAATAGATCCTTGCTCTGGATTCTCCCAATATGGAACCA 2236

RESULT 7
US-08-936-165A-87
Sequence 87, Application US/08936165A
Patent No. 6348582
GENERAL INFORMATION:
APPLICANT: Black, Michael
APPLICANT: Burnham, Martin
APPLICANT: Hodgson, John
APPLICANT: Knowles, David
APPLICANT: Lonetto, Michael
APPLICANT: Nicholas, Richard
APPLICANT: Pratt, Julie
APPLICANT: Reichard, Richard
APPLICANT: Rosenberg, Martin
APPLICANT: Ward, Judith
TITLE OF INVENTION: No. 6348582el Prokaryotic Polynucleotides,
TITLE OF INVENTION: Polypeptides and their Uses
NUMBER OF SEQUENCES: 534
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
COUNTRY: USA
ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/936,165A
FILING DATE: 24-SEP-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/027,032
FILING DATE: 24-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: Gimmi, Edward R.
REGISTRATION NUMBER: 38,891
REFERENCE/DOCKET NUMBER: P50549
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-4478
TELEFAX: 610-270-5090
TELEX:
INFORMATION FOR SEQ ID NO: 87:
SEQUENCE CHARACTERISTICS:
LENGTH: 656 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Genomic DNA
US-08-936-165A-87

Query Match 4.6%; Score 36.8; DB 4; Length 656;
Best Local Similarity 52.6%; Pred. No. 0.12;
Matches 80; Conservative 0; Mismatches 72; Indels 0; Gaps 0;

QY 392 CCAACGAGAAATTAATCTGTATATAAAGCGTAATTAATGTAAGAACTCCGATCGTTGG 451
DB 423 CCCAGGTGACGATCTACCTGTAATCGCTGTAGCATTAAAGCTTTAGAGCGCGATGC 482
QY 452 ACAAATATGAAAAATCTTCGAAATGCTTGAAGGAGTCAAGGACCTACTGCGTCCAG 511
DB 483 TCATACGAGAAAAATCTTAGAATTAATGGAAGCTGTAGATCTTACATTCCACTCCA 542
QY 512 GAAGCGATTTTGAATCCATCATCAAGGAAG 543
DB 543 GACGTGATCCTGACAAAACCAAGATGCCAG 574

RESULT 8
US-08-866-340-1/c
Sequence 1, Application US/08866340
Patent No. 6020318
GENERAL INFORMATION:
APPLICANT: Szyf, Moshe
APPLICANT: Bigey, Pascal
APPLICANT: Ramchandani, Shyam
TITLE OF INVENTION: DNA METHYLTRANSFERASE GENOMIC
TITLE OF INVENTION: SEQUENCES AND ANTISENSE OLIGONUCLEOTIDES
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
ADDRESSEE: HALE AND DORR LLP
STREET: 60 State Street
CITY: Boston
STATE: MA
COUNTRY: United States of America
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/866,340
FILING DATE:
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Keown, Wayne A.
REGISTRATION NUMBER: 33,923
REFERENCE/DOCKET NUMBER: 106.101.187
TELECOMMUNICATION INFORMATION:

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TELEPHONE: (617) 526-6000
TELEFAX: (617) 526-5000
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4084 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-866-340-1

Query Match
Best Local Similarity 4.5%; Score 35.8; DB 3; Length 4084;
Matches 82; Conservative 0; Mismatches 77; Indels 0; Gaps 0;

QY 319 TGGGAGGAACGTTACCAAGAGTCTTCTCGAGATGACCTAGAAATGCAGAGAAACAGCCT 378
DB 2865 TGGGTGACAGAGTGAGACTCTCTCAAAAAACAAAAACAAACAAAAACACCCAC 2806
QY 379 CCTCTCCCAAGCCACGAGAAATTAATGCTGATATAAAGCGTAATTAATGCTGAGGAC 438
DB 2805 CACCACCACTATTAGCAGCAAAATAGTCTGACATTAACAGAAATATCCAAATTATC 2746
QY 439 TCCGATGGCTTGGCAAAAAATATGAAAAATCTTCGAAA 477
DB 2745 TTGAACTCCATGGGAAAAATGCAAAATCCATTAAA 2707

RESULT 9
US-09-103-875-4/c
; Sequence 4, Application US/09103875A
; Patent No. 6221849
; GENERAL INFORMATION:
; APPLICANT: Syff, Moshe
; APPLICANT: Bigey, Pascal
; APPLICANT: Ramchandani, Shyam
; TITLE OF INVENTION: DNA METHYLTRANSFERASE GENOMIC SEQUENCES AND ANTISENSE
; TITLE OF INVENTION: OLIGONUCLEOTIDES
; FILE REFERENCE: 106101.194
; CURRENT APPLICATION NUMBER: US/09/103,875A
; CURRENT FILING DATE: 1998-06-24
; EARLIER APPLICATION NUMBER: 60/069,865
; EARLIER FILING DATE: 1997-12-17
; EARLIER APPLICATION NUMBER: 08/866,340
; EARLIER FILING DATE: 1997-05-30
; NUMBER OF SEQ ID NOS: 138
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 4460
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-103-875-4

Query Match
Best Local Similarity 4.5%; Score 35.8; DB 3; Length 4460;
Matches 82; Conservative 0; Mismatches 77; Indels 0; Gaps 0;

QY 319 TGGGAGGAACGTTACCAAGAGTCTTCTCGAGATGACCTAGAAATGCAGAGAAACAGCCT 378
DB 2863 TGGGTGACAGGTGAGACTCTCTCAAAAAACAAAAACAAACAAAAACACCCAC 2804
QY 379 CCTCTCCCAAGCCACGAGAAATTAATGCTGATATAAAGCGTAATTAATGTAAGGAAC 438
DB 2803 CACCACCACTATTAGAGCAAAATAGTCTGACATTAACAGAAATATCCAAATTATC 2744
QY 439 TCCGATGGCTTGGCAAAAAATATGAAAAATCTTCGAAA 477
DB 2743 TTGAACTCCATGGGAAAAATGCAAAATCCATTAAA 2705

RESULT 10
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US-08-809-254A-4/c
; Sequence 4, Application US/08809254A
; Patent No. 6660852
; GENERAL INFORMATION:
; APPLICANT: KESHI ET AL
; TITLE OF INVENTION: PROBE FOR DIAGNOSING INFECTIOUS DISEASES
; FILE REFERENCE: 19036/33767
; CURRENT APPLICATION NUMBER: US/08/809,254A
; CURRENT FILING DATE: 1997-05-16
; PRIOR APPLICATION NUMBER: PCT/JP95/02036
; PRIOR FILING DATE: 1995-10-02
; PRIOR APPLICATION NUMBER: JP 236348
; PRIOR FILING DATE: 1994-09-30
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 5829
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic probe
US-08-809-254A-4

Query Match
Best Local Similarity 4.3%; Score 34.2; DB 4; Length 5829;
Matches 45; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

QY 385 CCAAAAGCCCAACGAGAAATTAATGCTGATATAAAGCTAAATAGTGAAGGAACCTCCGAT 444
DB 3392 CAAAAGCAACTAGAAAGTTATGCTCAAAATAAAATCTAAATTTGACAATGTAAACCGAG 3333
QY 445 GCG 447
DB 3332 TCG 3330

RESULT 11
US-08-961-527-41
; Sequence 41, Application US/08961527
; Patent No. 6420135
; GENERAL INFORMATION:
; APPLICANT: Charles Kunsch
; TITLE OF INVENTION: Streptococcus pneumoniae Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 391
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/961,527
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Brookes, A. Anders
; REGISTRATION NUMBER: 36,373
; REFERENCE/DOCKET NUMBER: PB340P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 41:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9828 base pairs
```

```
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
US-08-961-527-41

Query Match
  4.3%; Score 34.2; DB 4; Length 9828;
Best Local Similarity 71.4%; Pred. No. 3.3;
Matches 45; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

QY 385 CCAAGCCACGAGAAATTAAGCTGATATAAAGTAAATAGTGAAGGAACTCCGAT 444
Db 4164 CAAAGCAAACTAGAAAGTATGCTCAAAATAAATCTAAATTTGCAATGTAACCGAG 4223
QY 445 GCG 447
Db 4224 TCG 4226

RESULT 12
US-09-543-681A-3279
; Sequence 3279, Application US/09543681A
; Patent No. 6605709
; GENERAL INFORMATION:
; APPLICANT: GARY BRETON
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS
; FILE REFERENCE: 2709.1002-001
; CURRENT APPLICATION NUMBER: US/09/543.681A
; CURRENT FILING DATE: 2000-04-05
; PRIOR FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 8344
; SEQ ID NO 3279
; LENGTH: 981
; TYPE: DNA
; ORGANISM: Proteus mirabilis
US-09-543-681A-3279

Query Match
  4.2%; Score 34; DB 4; Length 981;
Best Local Similarity 66.2%; Pred. No. 1.1;
Matches 49; Conservative 0; Mismatches 25; Indels 0; Gaps 0;

QY 414 ATAAAGCTAAATTAAGTGAAGGAACTCCGATGCGTTGGACAAATAATGAAAAATCTTC 473
Db 253 ATAAAAATAAATTAATTAAGGAGTTCGCTCTATTGCTCTGAAATGTAATAATATC 312
QY 474 GAAATGCTGAAG 487
Db 313 CAAATCGCAAGG 326

RESULT 13
US-09-621-976-15639/c
; Sequence 15639, Application US/09621976
; Patent No. 8639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET 054P22
; CURRENT APPLICATION NUMBER: US/09/621.976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 15639
; LENGTH: 505
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-621-976-15639

Query Match
  4.1%; Score 32.6; DB 3; Length 87350;
Best Local Similarity 49.7%; Pred. No. 34;
Matches 83; Conservative 0; Mismatches 84; Indels 0; Gaps 0;

QY 450 GGACAAAAATATGAAAAAATCTTCGAAATCTTGAAGGAGTGAAGGAGCCTACTGCAATC 509
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Matches 35; Conservative 123; Mismatches 127; Indels 0; Gaps 0;

QY 123 AAAAGGCAGAGATGGCCCTGTTGGCAAGAAACAAGAGAGAGAGACGCTTATTGCA 182
Db 401 AAMRGWECARGRTGSGWKGKGYRMGRGMAAKRMAAAGSYCGMITSYTSKRWIG 342
QY 183 GGCTCTGCATGTCACAAAGAAAGAACTTATGACAGACATGCTATTCCACCCAGCAA 242
Db 341 RKGWTKKRMVTVSGMWTYSYKCTKTKYTGKSKKTWTCTISWKYMMWMSGCWARS 282
QY 243 TTGATTTCTCAGATGATGATCTCACTGGTTTCAGCAAGATAGGATGATGCAAGAACCT 302
Db 281 MKSWARWYSWYMACWMSASAYRARSMTYCARRSWAGAGWWRARRGKRRGKSSMM 222
QY 303 GGTAGCAATGCACTGTGGGAGGAAAGCTTACACAGCAGTTTCTCTGAGATGACCTAGAA 362
Db 221 RSKMSWMSAGKARMCRRWMSCRMSYSCMSKSCRGTCXKMWRYARYAKRYASSM 162
QY 363 TGCAGAGAAACAGCTCTCTCCCAAAAGCAAGCAAGAAATTAAT 407
Db 161 GKYMWGRCWCYAKCARMYGYRSTRSTGSRGMYRRKMYMMK 117

RESULT 14
US-08-781-79/c
; Sequence 79, Application US/08781891
; Patent No. 6090620
; GENERAL INFORMATION:
; APPLICANT: Fu, Ying-Hui
; APPLICANT: Yu, Chang-En
; APPLICANT: Oshima, Junko
; APPLICANT: Mulligan, John T.
; APPLICANT: Schellenberg, Gerald D.
; TITLE OF INVENTION: GENE AND GENE PRODUCTS RELATED TO
; TITLE OF INVENTION: WERNER'S SYNDROME
; NUMBER OF SEQUENCES: 209
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED AND BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/781.891
; FILING DATE: 27-DEC-1996
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 6090620tenburg Ph.D., Carol
; REGISTRATION NUMBER: 39,317
; REFERENCE/DOCKET NUMBER: 240052.419
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 79:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 87350 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-781-891-79

Query Match
  4.1%; Score 32.6; DB 3; Length 87350;
Best Local Similarity 49.7%; Pred. No. 34;
Matches 83; Conservative 0; Mismatches 84; Indels 0; Gaps 0;

QY 450 GGACAAAAATATGAAAAAATCTTTCGAAATCTTGAAGGAGTGAAGGAGCCTACTGCAATC 509
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Search completed: April 26, 2004, 02:10:47
Job time : 41.687 secs

Db 49551 GAAGAAAAAATTTAAGAGAAATGAAGAAATAAAAAAGATGCAATGAAAAAGTGAATAA 49592
QY 510 AGGAAGCGATTTTGTATCATCATCAAGGAGCAGCAAGATGTATGAGACGAGACTTT 569
Db 49591 TTGAAGCTGGGTAAATGAAGATCCAAACATACATGTATAGCAGGAGTCTCTGAAGAAGAAAT 49532
QY 570 GTTAAAGCACTTAAAGAGAAATGAAGAGTATGATTTGAGATACCTT 616
Db 49531 ATGAAGTAATGGAATAAAACACTAAAGATATGATTTAAGAAAACTT 49485

RESULT 15

US-09-618-166-79/c

; Sequence 79, Application US/09618166

; Patent No. 6583112

; GENERAL INFORMATION:

; APPLICANT: Fu, Ying-Hui

; Yu, Chang-En

; Oshima, Junko

; Mulligan, John T.

; Schellenberg, Gerald D.

; TITLE OF INVENTION: GENE AND GENE PRODUCTS RELATED TO

; WERNER'S SYNDROME

; NUMBER OF SEQUENCES: 209

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Seed Intellectual Property Law Group

; STREET: 701 Fifth Avenue, Suite 6300

; CITY: Seattle

; STATE: Washington

; COUNTRY: USA

; ZIP: 98104-7092

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/618,166

; FILING DATE: 17-Jul-2000

; CLASSIFICATION: <Unknown>

; ATTORNEY/AGENT INFORMATION:

; NAME: McMasters, David D.

; REGISTRATION NUMBER: 33,963

; REFERENCE/DOCKET NUMBER: 240052.419C1

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (206) 622-4900

; TELEFAX: (206) 682-6031

; INFORMATION FOR SEQ ID NO: 79:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 87350 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; SEQUENCE DESCRIPTION: SEQ ID NO: 79:

US-09-618-166-79

Query Match 4.1%; Score 32.6; DB 4; Length 87350;
Best Local Similarity 49.7%; Pred. No. 34;
Matches 83; Conservative 0; Mismatches 84; Indels 0; Gaps 0;

QY 450 GGACAAAAATGAAAAATCTTCGAAATGCTTGAAGGAGTCCAAAGGACCTACTGCGATC 509
Db 49651 GAAGAAAAAATTTAAAGAGAAATGAAGAAATAAAAGATGCAATGCAAGTGAAGTGAATAA 49592

QY 510 AGGAAGCGATTTTGTATCATCATCAAGGAGCAGCAAGATGTATGAGACGAGACTTT 569
Db 49591 TTGAAGCTGGGTAAATGAAGATCCAAACATACATGTATAGCAGGAGTCTCTGAAGAAGAAAT 49532

QY 570 GTTAAAGCACTTAAAGAGAAATGAAGAGTATGATTTGAGATACCTT 616
Db 49531 ATGAAGTAATGGAATAAAACACTAAAGATATGATTTAAGAAAACTT 49485

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: April 24, 2004, 23:47:42 ; Search time 212.564 Seconds
(without alignments)
15988.422 Million cell updates/sec

Title: US-10-051-835-12

Perfect score: 800
Sequence: 1 ctctctccagcaggtcag.....taaaagatgtttttttccc 800

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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1: Geneseq1980s:*
2: Geneseq1990s:*
3: Geneseq2000s:*
4: Geneseq2001as:*
5: Geneseq2001bs:*
6: Geneseq2002s:*
7: Geneseq2003as:*
8: Geneseq2003bs:*
9: Geneseq2003cs:*
10: Geneseq2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	800	100.0	800	7 ABX77562	Abx77562 Different
2	800	100.0	800	8 ACD42209	Ac42209 Human put
3	768	96.0	1121	7 ABX76277	Abx76277 Lung canc
4	760	95.0	1121	7 ABX76278	Abx76278 Lung canc
5	748	93.5	1120	7 ABX76281	Abx76281 Lung canc
6	746.4	93.3	1120	7 ABX76279	Abx76279 Lung canc
7	716	89.5	1117	7 ABX76280	Abx76280 Lung canc
8	419	52.4	533	5 AAS76577	Aas76577 DNA encod
9	223.6	27.9	3812	7 AAS55710	Aas55710 CDNA enco
10	223.6	27.9	3812	8 ACA63028	Ac63028 Human cDN
11	187.6	23.4	2021	2 AAZ32204	Aaz32204 Human sdp
12	186	23.2	3045	7 ABZ18334	Abz18334 Group III
13	178.4	22.3	1914	6 ABS56938	Ab56938 cDNA enco
14	166	20.8	1222	6 ABZ70855	Abz70855 Human cys
15	157.6	19.7	3092	9 ABE06592	Ab6592 Novel cod
16	130	16.2	551	6 ABU83301	Ab83301 Human ova
17	127.4	15.9	366	5 AAS64431	Aa64431 DNA enco
18	99.6	12.4	1030	4 AA161041	Aa161041 Human pol
19	99.6	12.4	1085	4 AA159255	Aa159255 Human sdp
20	98.8	12.3	497	5 AAS76576	Aas76576 DNA enco
21	70.6	8.8	65042	7 AAS55711	Aas55711 DNA enco
22	70.6	8.8	65042	8 ACA63029	Ac63029 Human gen
23	69.8	8.7	2718	4 AAK94793	Aak94793 Human ful

ALIGNMENTS

RESULT 1

ABX77562
ID ABX77562 standard; cDNA; 800 BP.
XX
AC ABX77562;
XX
DT 09-APR-2003 (first entry)
XX
DE Differentially expressed breast cancer associated cDNA #57.
XX
KW Breast cancer; differential gene expression; BC-cDNA;
KW breast cancer diagnosis; breast cancer monitoring;
KW breast cancer treatment; breast cancer staging; gene; ss.
XX
OS Homo sapiens.
XX
PN US2002156263-A1.
XX
PD 24-OCT-2002.
XX
PF 04-OCT-2001; 2001US-00974298.
XX
PR 05-OCT-2000; 2000US-0238331P.
XX
PA (CHEN/) CHEN H.
XX
PI Chen H;
XX
DR WPI; 2003-182653/18.
XX
PT New cDNAs, which are differentially expressed in (metastatic) breast
PT cancer useful for diagnosing or staging, breast cancer, or for monitoring
PT the treatment of breast cancer in an individual.
XX
PS Claim 1; SEQ ID NO 69; 30pp; English.
XX
CC The invention describes a combination of cDNAs (designated BC-cDNAs),
CC which are differentially expressed in breast cancer. The combination
CC includes 152 cDNA sequences, or their complements. The protein encoded by
CC any of these BC-cDNAs is useful for screening several molecules or
CC compounds to identify at least one ligand that specifically binds the
CC protein, producing or preparing polyclonal or monoclonal antibodies, or
CC purifying antibodies from a sample. The antibodies, which specifically
CC bind the protein differentially expressed in breast cancer is useful for
CC detecting the expression of a protein in a sample. The BC-cDNAs are also
CC useful for diagnosing, monitoring the treatment of, or staging, breast

24 69.8 8.7 3690 6 AAL39862 DNA codin
25 69.8 8.7 3691 2 AAX99691 Nucleic a
26 69.8 8.7 3691 2 AAZ06408 Tumour su
27 61.6 7.7 204 2 AAZ32207 Human sdp
28 42.4 5.3 2000 7 ADA71938 Rice gene
29 41.8 5.2 3813 4 ABL12727 Drosophil
30 39.8 5.0 3552 7 ACA29200 Prokaryot
31 38.6 4.8 2000 7 ADA71938 Rice gene
32 37.2 4.7 6008 2 AQA41289 Ubiquitin
33 36.8 4.6 656 2 AAT83947
34 36.8 4.6 656 2 AAV53387 DNA encod
35 36.4 4.5 110000 7 ABZ79565.1
36 36.2 4.5 741 4 AAS31370
37 36.2 4.5 741 5 ABA13461 Human ner
38 36.2 4.5 741 6 ABO66694 Human pol
39 36.2 4.5 741 9 ADC10716 Human cDN
40 36.2 4.5 3027 6 ABO66534 Human cDN
41 36.2 4.5 3027 9 ADC10556 Human pol
42 36.2 4.5 3060 6 ABA59744 Novel hum
43 35.8 4.5 526 6 ABO32524 Oligonucl
44 35.8 4.5 526 6 ABO32525 Oligonucl
45 35.8 4.5 526 6 ABO32525 Oligonucl

QY 693 TTCTACAATGGAGCAGGATATTGCTGAAGTCTCTGGCATATGTTACCGAATCAAAATAGC 752
 Db 901 TTCTACAATGGAGCAGGATATTGCTGAAGTCTCTGGCATATGTTACCGAATCAAAATAGC 960
 QY 753 CTTCCAGAGCGCTAAGAAATTCCTGTAGTAAAGATGTTCTTTTCCC 800
 Db 961 CTTCCAGAGCGCTAAGAAATTCCTGTAGTAAAGATGTTCTTTTCCC 1008

RESULT 4

ID ABX76278 standard; DNA; 1121 BP.
 XX AC ABX76278;
 XX
 DT 02-APR-2003 (first entry)
 XX
 DE Lung cancer-associated polynucleotide #143.
 XX
 KW Lung cancer-associated polynucleotide; gene; ds; cytostatic; emphysema;
 KW antiinflammatory; antiaschmatic; non-small cell lung cancer; atelectasis;
 KW small cell lung cancer; benign lesion; precancerous lesion; bronchitis;
 KW chronic obstructive pulmonary disease; hypersensitivity pneumonitis;
 KW interstitial pulmonary fibrosis; fibrosis; asthma; bronchiectasis.
 XX
 OS Unidentified.
 XX
 PN WO200286443-A2.
 XX
 PD 31-OCT-2002.
 XX
 PF 18-APR-2002; 2002WO-US012476.
 XX
 PR 18-APR-2001; 2001US-0284770P.
 PR 10-MAY-2001; 2001US-0290492P.
 PR 09-NOV-2001; 2001US-0339245P.
 PR 13-NOV-2001; 2001US-0350666P.
 PR 25-NOV-2001; 2001US-0334370P.
 PR 12-APR-2002; 2002US-0372246P.
 XX
 PA (BOSB-) EOS BIOTECHNOLOGY INC.
 XX
 PI Aziz N, Murray R;
 XX
 DR WPI; 2003-093161/08.
 DR P-PSDB; ABUS6550.
 XX

PT Detecting a lung cancer-associated transcript in a cell from a patient
 PT for treating lung cancer, by contacting a biological sample from the
 PT patient with a polynucleotide that exhibits increased or decreased
 PT expression in lung cancer.

PS Claim 22; Page 297; 453pp; English.

XX The invention relates to a method for detecting a lung cancer-associated
 CC transcript in a cell from a patient, comprising contacting a biological
 CC sample from the patient with a polynucleotide that selectively hybridizes
 CC to a sequence that is at least 80 % identical to a gene that exhibits
 CC increased or decreased expression in lung cancer samples. Lung cancer-
 CC associated polynucleotides and polypeptides are used for identifying a
 CC compound that modulates a lung cancer-associated polypeptide, for
 CC inhibiting proliferation of a lung cancer-associated cell to treat lung
 CC cancer in a patient and for treating a mammal having lung cancer by
 CC administering a modulatory compound identified. The methods are useful
 CC for treating lung cancer, such as small cell lung cancer, non-small cell
 CC lung cancer or other benign or precancerous lesions, e.g. atelectasis,
 CC emphysema, bronchitis, chronic obstructive pulmonary disease, fibrosis,
 CC hypersensitivity pneumonitis, interstitial pulmonary fibrosis, asthma and
 CC bronchiectasis. The genes, polynucleotides and polypeptides are useful
 CC for diagnostic purposes and as targets for screening for therapeutic
 CC compounds that modulate lung cancer, such as antibodies. Sequences
 CC ABX76124-ABX76474 represent lung cancer-associated polynucleotides of the

CC invention

XX XX Sequence 1121 BP; 329 A; 244 C; 268 G; 280 T; 0 U; 0 Other;
 SQ Query Match 95.0%; Score 760; DB 7; Length 1121;
 Best Local Similarity 99.3%; Pred. No. 1.4e-225;
 Matches 763; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 QY 33 GAAACAATGACCGATATAAAGACAGAGAGAGTGGCTGTAGATCCTGAAACTGTGTTAAACGT 92
 Db 241 GAAACAATGACCGATATAAAGACAGAGAGAGTGGCTGTAGATCCTGAAACTGTGTTAAACGT 300
 QY 93 CCCAGGGAATGTGACAGTCTCTCGTATCAGAAAGGAGGAGATGCGCTGTGGCAAG 152
 Db 301 CCCAGGGAATGTGACAGTCTCTCGTATCAGAAAGGAGGAGATGCGCTGTGGCAAG 360
 QY 153 AAACAAGGAGCAGGACAGACGCTTATTGAGGCTCTGCCATGTCACAAAGAAAGAGCTT 212
 Db 361 AAACAAGGAGCAGGACAGACGCTTATTGAGGCTCTGCCATGTCACAAAGAAAGAGCTT 420
 QY 213 ATGACAGGACATGCTATTCCACCCAGCCAAATTCAGATTGATGACTTCACTGGT 272
 Db 421 ATGACAGGACATGCTATTCCACCCAGCCAAATTCAGATTGATGACTTCACTGGT 480
 QY 273 TTCAGCAAAAGATAGGATGATGACAGAAACCTGTAGCAATGCACTGTGGAGGAAACGTT 332
 Db 481 TTCAGCAAAAGATAGGATGATGACAGAAACCTGTAGCAATGCACTGTGGAGGAAACGTT 540
 QY 333 ACCAGCAGTTTCTCTGGAGATGACCTAGATGACAGAGAAACAGCCTCTCTCCCAAAAGC 392
 Db 541 ACCAGCAGTTTCTCTGGAGATGACCTAGATGACAGAGAAACAGCCTCTCTCCCAAAAGC 600
 QY 393 CAACGAGAAATTAATGCTGATATATAAAGCTTAATAGTGAAGAACTCCGATCGTTGGA 452
 Db 601 CAACGAGAAATTAATGCTGATATATAAAGCTTAATAGTGAAGAACTCCGATCGTTGGA 660
 QY 453 CAAAATATGAAAATAATCTTCGAATGCTTGAAGGAGTGAAGGAGTCACTGCAAGTCAGG 512
 Db 661 CAAAATATGAAAATAATCTTCGAATGCTTGAAGGAGTGAAGGAGTCACTGCAAGTCAGG 720
 QY 513 AAGCGATTTTTTGAATCCATCATCAAGGAGCAGCAAGATGATAGACGAGACTTTGTT 572
 Db 721 AAGCGATTTTTTGAATCCATCATCAAGGAGCAGCAAGATGATAGACGAGACTTTGTT 780
 QY 573 AAGCACCCTTAAGAGAAACTGAAACGATATGATTGGAATACCTTGTCCCTGGAGGATTAT 632
 Db 781 AAGCACCCTTAAGAGAAACTGAAACGATATGATTGGAATACCTTGTCCCTGGAGGATTAT 840
 QY 633 CACACCCCAATGCAATATCTCGTTAATGATTGAGGAGAGAGAAAGGATCAGATTGCTGTT 692
 Db 841 CACACCCCAATGCAATATCTCGTTAATGATTGAGGAGAGAGAGAAAGGATCAGATTGCTGTT 900
 QY 693 TTCTACAATGGAGCAGGATATTGCTGAAGTCTCTGGCATATGTTACCGAATCAAAATAGC 752
 Db 901 TTCTACAATGGAGCAGGATATTGCTGAAGTCTCTGGCATATGTTACCGAATCAAAATAGC 960
 QY 753 CTTCCAGAGCGCTAAGAAATTCCTGTAGTAAAGATGTTCTTTTCCC 800
 Db 961 CTTCCAGAGCGCTAAGAAATTCCTGTAGTAAAGATGTTCTTTTCCC 1008

RESULT 5

ABX76281
 ID ABX76281 standard; DNA; 1120 BP.
 XX AC ABX76281;
 XX
 DT 02-APR-2003 (first entry)
 XX
 DE Lung cancer-associated polynucleotide #146.
 XX Lung cancer-associated polynucleotide; gene; ds; cytostatic; emphysema;
 KW antiinflammatory; antiaschmatic; non-small cell lung cancer; atelectasis;
 KW

KW small cell lung cancer; benign lesion; precancerous lesion; bronchitis;
 KW chronic obstructive pulmonary disease; hypersensitivity pneumonitis;
 KW interstitial pulmonary fibrosis; fibrosis; asthma; bronchiectasis.
 XX Unidentified.
 OS
 PN WO200286443-A2.
 XX
 PD 31-OCT-2002.
 XX
 PF 18-APR-2002; 2002WO-US012476.
 XX
 PR 18-APR-2001; 2001US-0284770P.
 PR 10-MAY-2001; 2001US-0290492P.
 PR 09-NOV-2001; 2001US-0339245P.
 PR 13-NOV-2001; 2001US-0350666P.
 PR 29-NOV-2001; 2001US-0334370P.
 PR 12-APR-2002; 2002US-0372246P.
 XX
 PA (EOB-) EOS BIOTECHNOLOGY INC.
 XX
 PI Aziz N, Murray R;
 XX
 DR WPI: 2003-093161/08.
 DR P-PSDB; ABUS6553.
 XX
 PT Detecting a lung cancer-associated transcript in a cell from a patient
 PT for treating lung cancer, by contacting a biological sample from the
 PT patient with a polynucleotide that exhibits increased or decreased
 PT expression in lung cancer.
 XX
 PS Claim 22; Page 298; 453pp; English.
 XX
 CC The invention relates to a method for detecting a lung cancer-associated
 CC transcript in a cell from a patient, comprising contacting a biological
 CC sample from the patient with a polynucleotide that selectively hybridises
 CC to a sequence that is at least 80 % identical to a gene that exhibits
 CC increased or decreased expression in lung cancer samples. Lung cancer-
 CC associated polynucleotides and polypeptides are used for identifying a
 CC compound that modulates a lung cancer-associated polypeptide, for
 CC inhibiting proliferation of a lung cancer-associated cell to treat lung
 CC cancer in a patient and for treating a mammal having lung cancer by
 CC administering a modulatory compound identified. The methods are useful
 CC for treating lung cancer, such as small cell lung cancer, non-small cell
 CC lung cancer or other benign or precancerous lesions, e.g. atelectasis,
 CC emphysema, bronchitis, chronic obstructive pulmonary disease, fibrosis,
 CC hypersensitivity pneumonitis, interstitial pulmonary fibrosis, asthma and
 CC bronchiectasis. The genes, polynucleotides and polypeptides are useful
 CC for diagnostic purposes and as targets for screening for therapeutic
 CC compounds that modulate lung cancer, such as antibodies. Sequences
 CC ABX76124-ABX76474 represent lung cancer-associated polynucleotides of the
 CC invention
 XX
 SQ Sequence 1120 BP; 329 A; 243 C; 266 G; 282 T; 0 U; 0 Other;
 Query Match 93.5%; Score 748; DB 7; Length 1120;
 Best Local Similarity 99.2%; Pred. No. 7.4e-222;
 Matches 762; Conservative 0; Mismatches 5; Indels 1; Gaps 1;
 33 GAAACATGACCCGATGAAACAGAGAGGCTGCTAGATCCTGAACTGTGTTAACT 92
 241 GAAACATGACCCGATGAAACAGAGAGGCTGCTAGATCCTGAACTGTGTTAACT 300
 93 CCCAGGGAATGTGACAGTCTTCTGATCAGAAAAGGAGGAGGATGCCCTGTGGCAAG 152
 301 CCCAGGGAATGTGACAGTCTTCTGATCAGAAAAGGAGGAGGATGCCCTGTGGCAAG 360
 153 AAACAGGAGCAGGAGACGCTTATGCGGCTCTGCCATGCTCCAAAGAAAGAGCTT 212
 361 AAACAGGAGCAGGAGACGCTTATGCGGCTCTGCCATGCTCCAAAGCAAG-AGCTT 419
 213 ATGACAGGACATGCTATTCACCCAGCCAAATGGATTCTCAGATTGATGACTTCACTGT 272

420 ATGACAGGACATGCTATTCCACCCAGCCAAATGGATTCTCAGATTGATGACTTCACTGGT 479
 273 TTGAGCAAAAGATAGGATGATGCAAAAACCTGGTAGCAATGCACTCTGGGAGGAAACGTT 332
 480 TTGAGCAAAAGATAGGATGATGCAAAAACCTGGTAGCAATGCACTCTGGGAGGAAACGTT 539
 333 ACCAGCAGTTTCTCTGGAGATGACCTAGATGACAGAGAAACAGCCCTCTCTCCAAAAGC 392
 540 ACCAGCAGTTTCTCTGGAGATGACCTAGATGACAGAGAAACAGCCCTCTCTCCAAAAGC 599
 393 CAACGAGAAATTAATGCTGATATAAAACGTAATAATAGTGAAGAACTCCGATCGGTGGA 452
 600 CAACGAGAAATTAATGCTGATATAAAACGTAATAATAGTGAAGAACTCCGATCGGTGGA 659
 453 CAAAATATCAAAAATATCTTCGAAATCTTTGAAGAGTGAAGAGCTTCTGAGTCAAGCAG 512
 660 CAAAATATCAAAAATATCTTCGAAATCTTTGAAGAGTGAAGAGCTTCTGAGTCAAGCAG 719
 513 AAGCGATTTTGAATCCATCATCAAGGAGCAGCAAGATGATGAGACGAGACTTTGTT 572
 720 AAGCGATTTTGAATCCATCATCAAGGAGCAGCAAGATGATGAGACGAGACTTTGTT 779
 573 AAGCACCTTTAAGAGAAACTGAAACGTTATGATTGAGAAATCTTGTCCTCGGAGGATTAT 632
 780 AAGCACCTTTAAGAGAAACTGAAACGTTATGATTGAGAAATCTTGTCCTCGGAGGATTAT 839
 633 CAGACCCCAATGCAATCTCTGTTAATGATTGAGGAGGAGAAAGGATCAGATTGCTGTT 692
 840 CAGACCCCAATGCAATCTCTGTTAATGATTGAGGAGGAGAAAGGATCAGATTGCTGTT 899
 693 TTCTACAAATGGAGCAGGATATTGCTGAAGTCTCTCTGTCATATGTTACCGAATCAAAATAGC 752
 900 TTCTACAAATGGAGCAGGATATTGCTGAAGTCTCTCTGTCATATGTTACCGAATCAAAATAGC 959
 753 CTTCAGAGCTAAGAAATTTCTGTTAGTAAAGATGTTCTTTTCCC 800
 960 CTTCAGAGCTAAGAAATTTCTGTTAGTAAAGATGTTCTTTTCCC 1007
 RESULT 6
 ABX76279
 1D ABX76279 standard; DNA; 1120 BP.
 XX
 AC ABX76279;
 XX
 DT 02-APR-2003 (first entry)
 XX
 DE Lung cancer-associated polynucleotide #144.
 XX
 DE Lung cancer-associated polynucleotide; gene; ds; cytostatic; emphysema;
 XX antiinflammatory; antiasthmatic; non-small cell lung cancer; atelectasis;
 XX small cell lung cancer; benign lesion; precancerous lesion; bronchitis;
 XX chronic obstructive pulmonary disease; hypersensitivity pneumonitis;
 XX interstitial pulmonary fibrosis; fibrosis; asthma; bronchiectasis.
 XX
 OS Unidentified.
 XX
 PN WO200286443-A2.
 XX
 PD 31-OCT-2002.
 XX
 PF 18-APR-2002; 2002WO-US012476.
 XX
 PR 18-APR-2001; 2001US-0284770P.
 PR 10-MAY-2001; 2001US-0290492P.
 PR 09-NOV-2001; 2001US-0339245P.
 PR 13-NOV-2001; 2001US-0350666P.
 PR 29-NOV-2001; 2001US-0334370P.
 PR 12-APR-2002; 2002US-0372246P.
 XX
 PA (EOB-) EOS BIOTECHNOLOGY INC.
 XX
 PI Aziz N, Murray R;

QY 562 GAGACTTTGTTAAGCACTTAAGAGAACTGAAGCGTATGATTTGAGAAATCTTGTCCC 621
DB 353 GAGACTTTGTTAAGCACTTAAGAGAACTGAAGCGTATGATTTGAGAAATCTTGTCCC 294
QY 622 TGGAGGATTATCACACCCCAATGCTAATCTGTTAATGATTGAGGAGAGAAAAGGATC 681
DB 293 TGGAGGATTATCACACCCCAATGCTAATCTGTTAATGATTGAGGAGAGAAAAGGATC 234
QY 682 AGATTGCTGTTTCTACATGAGGAGGAGGATATGCTGAAAGTCTCTCGGCATATGTTACCG 741
DB 233 AGATTGCTGTTTCTACATGAGGAGGAGGATATGCTGAAAGTCTCTCGGCATATGTTACCG 174
QY 742 AATCAATAGCTTCCAGAGGCTTAAGAAATTTCTGTAGTAAAGATGTTCTTTTCCC 800
DB 173 AATCAATAGCTTCCAGAGGCTTAAGAAATTTCTGTAGTAAAGATGTTCTTTTCCC 115
RESULT 9
ID ABS55710
XX ABS55710 standard; cDNA; 3812 BP.
AC ABS55710;
XX
DT 17-JAN-2003 (first entry)
XX
XX cDNA encoding novel human deleted in cancer 1 (DICE1) like protein.
XX Human; deleted in cancer 1; DICE1; helicase family; carcinoma;
XX transgenic animal; ribozyme design; drug screening; gene therapy;
XX tumour suppressor; gene; ss.
XX Homo sapiens.
XX Key Location/Qualifiers
FH 321..2906
FT CDS /tag= a
FT /product= "DICE1"
FT /notes= "Deleted in cancer 1 like protein"
XX
XX US2002128188-A1.
XX
XX 12-SEP-2002.
XX
XX 16-FEB-2001; 2001US-00784316.
XX
XX 16-FEB-2001; 2001US-00784316.
XX
XX (WEIM/) WEI M.
XX (YEJ/) YE J.
XX (KETC/) KETCHUM K A.
XX (DFRA/) DI FRANCESCO V.
XX (BEAS/) BEASLEY E M.
XX
XX Wei M, Ye J, Ketchum KA, Di Francesco V, Beasley EM;
XX WPI; 2003-039599/03.
XX P-PSDB; ABG7111.
XX
XX Novel human enzyme protein, related to helicase subfamily, useful as
XX model for developing human therapeutic targets and serves as target for
XX human therapeutics.
XX
XX Claim 22; Fig 1; 86pp; English.
XX
XX The invention describes an isolated human enzyme peptide (I) that is
XX related to the helicase family. (I), its allelic variant, orthologue or
XX fragment is useful for identifying a modulator of a human enzyme peptide.
XX The method optionally involves contacting a cell expressing the peptide
XX with an agent and determining if the agent has modulated the expression
XX of the peptide. (I) and the polynucleotide encoding it (iii) can be used
XX as models for the development of human therapeutic targets, aid in the
XX identification of therapeutic proteins and serve as targets for the
XX development of human therapeutic agents that modulate enzyme activity in

CC cells and tissue that express the enzyme. The proteins can also be used
CC in screening assays to screen a compound for its ability to stimulate or
CC inhibit interaction between enzyme protein and a molecule that normally
CC interacts with the enzyme protein. The proteins also provide a target for
CC diagnosing a disease or predisposition to disease mediated by the
CC peptide, and in pharmacogenomic analysis. The peptides are also useful
CC for treating a disorder characterised by altered expression of the
CC protein e.g. carcinoma. Anti-(I) antibodies are also useful for assessing
CC normal and aberrant subcellular localisation of cells in various tissues
CC in an organism, in pharmacogenomic analysis, for tissue typing and for
CC inhibiting protein function. The nucleic acid molecules are useful for
CC constructing recombinant vectors, host cells and transgenic animals, and
CC for designing ribozymes. The nucleic acids are also useful in drug
CC screening assays and as a target for treatment by the compounds
CC identified through drug screening. The nucleic acid molecules are also
CC useful in diagnostic assays for qualitative changes in expression of
CC nucleic acid encoding enzyme and particularly in qualitative changes that
CC lead to pathology. Detection of mutated form of gene encoding enzyme
CC associated with a dysfunction provides a diagnostic tool for a active
CC disease or susceptibility to disease which results from altered
CC expression of enzyme protein. (iii) also provides vectors for gene
CC therapy in patients with aberrant expression of gene encoding enzyme.
CC This sequence encodes the novel human protein deleted in cancer 1 (DICE1)
CC like protein, a candidate tumour suppressor gene
XX
SQ Sequence 3812 BP; 1169 A; 796 C; 840 G; 1007 T; 0 U; 0 Other;
Query Match 27.9%; Score 223.6; DB 7; Length 3812;
Best Local Similarity 64.6%; Pred. No. 1.9e-58;
Matches 384; Conservative 0; Mismatches 174; Indels 36; Gaps 2;
QY 212 TATGACAGGACATGCTATTCACCCAGCCCAATGGATTTCTCAGATTGAGCTTCACTGG 271
DB 2429 TATGACAGGAGATCTTATGCCACCCCAACCAAGTGGATTTCTCTCTGACGACTTCAAG 2488
QY 272 TTTCAGCAAGATAGGATGATGAGAAACCTGTAGCAATGCACCTGTGGAGGAAACGT 331
DB 2489 TCTCAGCAAGATAGGCTGATTCAGAAACCTGTAGTACGATTTGTAGGAGGACCAA 2548
QY 332 TACCAGCAGTTTCTCTGGAGATGACCTAGAAATGCAGAGAAACAGCCTC----- 379
DB 2549 AAACCTGAGTCTCTCCGTAGATGACCAAAAGACCCAGTAGCATCTACTTTGGAGGCTAT 2608
QY 380 -----CTCTCCAAAGCCCAACGAGAAATTAATGCTGATATAAAACG 421
DB 2609 GCCAATATACATTAATCAATCACTCTGCTATGGCAGAGGATCAATGCTGATATAAACA 2668
QY 422 TAAATTAGTGAAGAACTCCGATGCGGTGGACAAAATATGAAAAAATCTTGGAAATGCT 481
DB 2669 TCAATTAATGAAGGAGTTCCGAAAGTTTGGTCCGAAATATGAAAGAAATTTTCAATTTGCT 2728
QY 482 TGAAGGAGTGCAGGACCTACTGACGTCAGGAAGCGGATTTTGAATCCATCATCAAGGA 541
DB 2729 TGAAGAGTGCAGGACCTCTGGAGATGAAGAAACAGTTTGTGTAATTTACCATCAAGGA 2788
QY 542 AGCAGCAAGATGTATGAGACGAGACTTTGTTAAGCACCTTAAAGAGAAACTGGAACGATAT 601
DB 2789 AGCCGCAAGGTTTAAAGACGAGTCTCTAATTCAGTACCTTGAAGAGGTACTAGAAAAAT 2848
QY 602 GATTTGAGATATCTGTCTCCCTGGAGGATATACACCCCAATGCATATCTCGTTAATG 661
DB 2849 AATTTCCACACCTTCCACAAACACATTAGTCATCAACAGCAGATCATCATTTAGTG 2908
QY 662 -----ATTGAGGAGAGAAAAAGGATCAGATTGCTGTTTTTCTACAATGGAGCAGGATATTG 715
DB 2909 CAAAGACCAAGTGAAGAAAAAATGACAAAGTTTCTGTGCTGTAGGATGGAACAGGATATTG 2968
QY 716 CTGAAGTCTCTGTCATATGTTACCGGATCAATAGCTTCCAGAGGCTTAAGAA 769
DB 2969 TTGAAGGCTCTCTGGAATGTTTGTAGTCAAGGGAATTCGTTTCCAGATGCTTAAGAA 3022
RESULT 10

ACA63028
ID ACA63028 standard; cDNA; 3812 BP.
AC
AC ACA63028;
XX
XX
XX 25-AUG-2003 (first entry)
XX
XX Human cDNA encoding a DICE-1-like RNA helicase.
XX
XX Human; ss; gene; RNA helicase; DICE-1; deleted in cancer 1;
KW tumour suppressor gene; chromosome X; gene therapy; cytostatic.
XX
XX Homo sapiens.
XX
XX
XX Key Location/Qualifiers
FH 1..320
FT 5'UTR *tag= a
FT CDS 321..2906
FT *tag= b
FT /product= "DICE-1-like protein"
FT 2907..3812
FT 3'UTR *tag= c
XX
XX US2003013168-A1.
XX
XX 16-JAN-2003.
XX
XX 28-AUG-2002; 2002US-00229124.
XX
XX 16-FEB-2001; 2001US-00784316.
XX
XX (APPL-) APPLERA CORP.
XX
XX Wei M, Ye J, Ketchum KA, Di Francesco V, Beasley EM;
XX
XX WPI: 2003-491970/46.
XX P-PSDB; ABU61992.

New isolated human enzyme proteins, useful as models for developing human therapeutic targets, aid in identifying therapeutic proteins, or for diagnosing, treating or preventing enzyme protein-related conditions, e.g. carcinomas.

Claim 4; Fig 1; 90pp; English.

The invention relates to a new protein, human DICE1-like RNA helicase (deleted in cancer 1, a tumour suppressor gene). The protein may be an allelic variant or orthologue encoded by a nucleic acid molecule that hybridises under stringent conditions to the cDNA and gene appearing as ACA63028 and ACA63029, or a fragment of the protein of at least 10 amino acids. Also included are an antibody selectively binding to the helicase, a gene chip comprising nucleic acids, a transgenic non-human animal comprising the nucleic acid molecule, a nucleic acid vector comprising the nucleic acid molecule, a host cell containing the vector, identifying the protein or nucleic acids in a sample, identifying agents that bind to and/or modulate the activity of the protein (or expression of the nucleic acids), treating a disease or condition mediated by a human enzyme protein, an isolated human enzyme peptide having an amino sequence that shares at least 70% homology with the helicase and an isolated nucleic acid molecule encoding a human enzyme peptide, where the nucleic acid molecule shares at least 80% homology with the cDNA or gene. The methods are useful for detecting the presence of any of the claimed peptides, a nucleic acid molecule, a modulator of a peptide, an agent that binds to any of the peptides, and for identifying a modulator of expression of a peptide. The methods are also useful for treating a disease or condition mediated by a human enzyme protein. The human enzyme peptides and nucleic acid molecules are useful as models for developing human therapeutic targets, aid in the identification of therapeutic proteins, or as targets for the development of human therapeutic agents that modulate enzyme activity in cells and tissue that express the enzyme. They are useful in the diagnosis, prevention and treatment of enzyme protein-related conditions or disorders associated with the absence of, inappropriate, or unwanted expression of the protein, e.g. carcinomas. The peptides or

CC proteins may be used in drug screening assays, in assays to determine the biological activity of the protein, to raise antibodies or to elicit another immune response, as a reagent in assays designed to quantitatively determine levels of the protein in biological fluids, or as markers for tissues in which the corresponding protein is preferentially expressed. The nucleic acid molecules are useful as probes, primers, chemical intermediates, or in biological assays. The gene for the helicase is located on chromosome X. The present sequence is the cDNA encoding the DICE-1-like helicase

XX Sequence 3812 BP; 1169 A; 796 C; 840 G; 1007 T; 0 U; 0 Other;

Query Match 27.9%; Score 223.6; DB 8; Length 3812;
Best Local Similarity 64.6%; Pred. NO. 1.9e-58;
Matches 384; Conservative 0; Mismatches 174; Indels 36; Gaps 2;

QY	212	TATGACAGGACATGCTATTCCACCCAGCAATTCAGATTGAGTTCACCTCG	271
DB	2429	TATGACAGGAGATCTTATGCCACCAACCAAGTGGATTCTCTGTGACGATTCACAAG	2488
QY	272	TTTCAGCAAGATAGGATGATGCGAGAACTGTGTAGCAATGCACCTGTGGAGGAACTG	331
DB	2489	TCTCAGCAAGATGGGCTGATTCAAAACCTGTGTAGTACGCAATTTGTAGGAGGACCAA	2548
QY	332	TACCAGCAGTTTCTCTGGAGATGACCTAGATTGACAGAAACAGCCCTC	379
DB	2549	AAACTGCGATCTCTCGTAGATGACCAAAAGACCCAGTAGCATCTACTTTGGAGCTAT	2608
QY	380	-----CTCTCCAAAAGCCAAACGAGAAATTAATGCTGATATAAACG	421
DB	2609	GCCAAATACATTACAAATCACTCTCTATGGCACAAGGAATCAATGCTGTATATAAAC	2668
QY	422	TAAATTAGTGAAGCACTCCGATGCGTTGGACAAAATATGAAAAATCTTCGAAATGCT	481
DB	2669	TCAATTATGAAGAGTTCGAAAGTTTGTGCGAAATATGAAGAATTTTCATTTTGTCT	2728
QY	482	TGAAGGAGTCCAAAGGACCTACTCCAGTCAGGAGCGATTTTGAATCCCATCATCAAGGA	541
DB	2729	TGAAGAGTCCAAAGGACCTCTGGAGATGAAGAACAGTTTGTGAATTTACCATCAAGGA	2788
QY	542	AGCAGCAGATGTATGACGAGACCTTTGTAGCACCTTTAAGAAGAACTGGAACCTAT	601
DB	2789	AGCCGCAAGGGTTAAAGACGAGTCTTAATTCAGTACCTTGAGAGGATCTAGAAAAAT	2848
QY	602	GATTTGAGAACTCTGTCTCTGGAGGATTATCACACCCCAATGCATTAATCTCGTTAATG	661
DB	2849	AAATTCCACCACTTCAACCAACATTAAGTACATCAACAGCAGATCATCATGTTAGTG	2908
QY	662	-----ATTGAGGAGAGAAAGGATCAGATGCTGTTTCTACAAATGGAGCAGATATG	715
DB	2909	CAAGACCCAGTGAGAAAAAATGCAAGTTTCTGTCTGTAGATGGAAACAGATATG	2968
QY	716	CTGAAGTCTCTGGCATATGTTACCGAATCAATAGCTTTCCAGAGGCTAAGAA	769
DB	2969	TTGAAGCTCTGGAATGTTTGAAGTCAAGGAATGCTTTCCAGATGCTAAGAA	3022

RESULT 11

AAZ32204

ID AAZ32204 standard; cDNA; 2021 BP.

XX AAZ32204;

AC AAZ32204;

XX 14-JAN-2000 (first entry)

XX Human sdph3.10 (SAGE) encoding cDNA.

XX Human; sdph3.10; SAGE; sdp3.8; HAGE; sdp3.5; TRAP; sarcoma;

XX tumour rejection antigen precursor; tumour associated nucleic acid;

XX carcinoma; cancer; immune response; diagnosis; ss.

XX Homo sapiens.

OS

XX

FH Key Location/Qualifiers
 FT CDS 119..1834
 FT /*tag= a
 FT /product= "sdph3.10 (SAGE)"
 XX WO9953061-A2.
 XX 21-OCT-1999.
 XX 14-APR-1999; 99WO-US008163.
 XX 15-APR-1998; 98US-00060706.
 PR 27-JUL-1998; 98US-00122989.
 PR 30-OCT-1998; 98US-00183706.
 PR 30-OCT-1998; 98US-00183789.
 XX (LUDW-) LUDWIG INST CANCER RES.
 XX Martelange V, De Smet C, Boon-Falleur T;
 XX WPI; 1999-620430/53.
 XX P-PSDB; AAY49634.
 XX New nucleic acid encoding sarcoma-associated gene products, useful for
 PT diagnosing, e.g. treating and preventing cancer.
 XX Claim 1; Page 79-81; 93pp; English.
 XX The present sequence encodes human sdph3.10 (SAGE), a sarcoma-associated
 CC gene product (I). Agents, specifically sarcoma associated nucleic acids
 CC (II) or their expression products that are tumour rejection antigens
 CC (TRA), that selectively increase formation of HLA (human leucocyte
 CC antigen)/(II) complexes are used for treating cancer, especially sarcoma
 CC and carcinoma, in humans and other animals. Compositions containing
 CC autologous cytolytic T cells (CTL), specific for the HLA/(I) complex, are
 CC similarly useful, also transformed cells that stimulate such CTL in vivo.
 CC (II) are also used. (3) as source of therapeutic antisense sequences that
 CC reduce expression of (II); (ii) for recombinant production of (I); (iii)
 CC particularly its fragments, as primers and probes in usual hybridisation
 CC and amplification assays, for diagnosis, prognosis and monitoring of
 CC tumours; (iv) for measuring binding specificity of HLA molecules or CTL
 CC clones; (v) to identify related sequences; and (v) for generating
 CC transgenic animals, e.g. for studying cancer and immune responses to it.
 CC (I) are used to raise specific antibodies (Ab) and therapeutically. Ab
 CC are used to diagnose tumours in immunoassays, also for delivering drugs,
 CC toxins, imaging agents etc. to (I)-expressing cells
 XX
 SQ Sequence 2021 BP; 559 A; 436 C; 429 G; 497 T; 0 U; 0 Other;
 Query Match 23.4%; Score 187.6; DB 2; Length 2021;
 Best Local Similarity 60.2%; Pred. No. 2.2e-47;
 Matches 365; Conservative 0; Mismatches 209; Indels 32; Gaps 2;
 QY 195 TCACAGAGAAAGAGCTTATGACAGGACATGCTATTCCACCAGCCAAATGGATTCTCAG 254
 DB 1349 TCACAGAGCTGATAAATATATACAGGACATGTATGCCACCCCAATGCAATGATTCTTC 1408
 QY 255 ATTGATGACTTCACTGGTTTCAGCAAGATAGGATGATGAGAAACCTGTAGCAATGCA 314
 DB 1409 TCTCAGCACTTCAAGTCTCAGCAAGATGAGCTGTTTACAACTGATGATGAA 1468
 QY 315 CCTGTGGAGAAACGTTTACCAGCAGTTCTCTGGAGATGACCTAGATGTCAGAGAAACA 374
 DB 1469 TTTGCGGTAGGCACCAAAACTACAGTGTCTCTGCAGGTGACCCAGCTACAGTAATG 1528
 QY 375 GCCTC-----CTCTCCCAAGCCACAGCAAT 404
 DB 1529 TCTTCGGTGAACCTGTGCCAATACACCAAAATATCTCTGCTGCGCAAAAAT 1588
 QY 405 AATGCTGATATAACCGTAATTAAGTGAAGAACTCCGATGCGTTGGACAAAATATGAA 464
 DB 1589 AATGATGATATAAATATCAATTAATGAAGAACTTCGAAGTTTGGCGCAAAATATGAA 1648

QY 465 AAAATCTTCGAAATGCTTGAAGGAGTCAAGGACCTACTACTCAGTCAGGAAGCGATTTTT 524
 DB 1649 AGAATTTTCAATTTTGTGTTGAAGAGGTACAAGGATCTATGAAGTCAAGACAAATTTGTT 1708
 QY 525 GAATCCATCATCAGGAGGAGCAGCAAGATGATGAGACGAGACTTTGTTAAGCACTTTAAG 584
 DB 1709 GAATTTACCATCAAGGAGGAGCAGCAAGGTTTAAAAAGTTGTTCTTAATTCAGCACTGAG 1768
 QY 585 AAGAACTGAAACGTTATGATTTGAGAAATCTGTCCCTGGAGGATTTATCATACCCCCAAAT 644
 DB 1769 AAGCGGCTTAAAGAAATAGATTCCCACTGCCATCTCAGAAAAGTTAAGCACATGAGAAA 1828
 QY 645 GCATAATCTCGTTAATGATTTGAGAAATCTGTCCCTGGAGGATTTATCATACCCCCAAAT 704
 DB 1829 AGATAATTTGTTAGTG--CAAGACCAAGGAGAAACAGACATATGCTGTAGGATGGA 1886
 QY 705 GCAGGATATTGCTGAAGTCTCTGGGCATATGTTACCGAATCAATAGCCCTTCAGAGGCT 764
 DB 1887 ACAGGTTATTGCTGAAGTCTCTGATAATCTGAAATGAAGAGAATCCCTTCCAGAGCT 1946
 QY 765 AAGAAA 770
 DB 1947 ACGAAA 1952
 RESULT 12
 ABZ18334
 ID ABZ18334 standard; cDNA; 3045 BP.
 XX AC ABZ18334;
 XX DT 23-JAN-2003 (first entry)
 XX DE Group III cDNA cancer related clone SEQ ID NO:760.
 XX KW Human; cancer; tumour; therapy; diagnosis; CT antigen; CP antigen;
 KW immune response; virology; immunology; microbiology; molecular biology;
 KW recombinant DNA technology; gene; ss.
 XX OS Homo sapiens.
 XX PN WO200278516-A2.
 XX PD 10-OCT-2002.
 XX PF 28-MAR-2002; 2002WO-US010421.
 XX PR 30-MAR-2001; 2001US-0280255P.
 PR 28-AUG-2001; 2001US-0315563P.
 PR 09-JAN-2002; 2002US-0347313P.
 XX PA (CORI-) CORIYA CORP.
 XX PI Wang T, Wang S, Bangur CS, Gaiger A;
 XX WPI; 2003-058387/05.
 PT New immunogenic polynucleotides or polypeptides useful for diagnosing,
 PT preventing and treating cancer expressing CT or CP mRNA antigens, and in
 PT virology, immunology, microbiology, molecular biology and recombinant DNA
 PT techniques.
 XX Claim 1; SEQ ID NO 760; 207pp; English.
 CC ABQ17575 to ABQ20506 represent isolated polynucleotide (I) sequences, and
 CC ABP5446 to ABP54472 represent protein (II) sequences, from the present
 CC invention. (I) and (II) have cytostatic activity and can be used in gene
 CC therapy and vaccines. (I), (II), antibodies and compositions from the
 CC present invention are useful for diagnosing, preventing and treating
 CC cancer, which expresses CT or CP mRNA antigens. They are useful for
 CC stimulating immune response. They can also be useful in virology,
 CC immunology, microbiology, molecular biology and recombinant DNA
 CC techniques. N.B. The sequence data for this patent did not form part of

XX
XX
XX
/PRODUCT= human DICER-50-01.2.7 PROGRAM

AA 14-APR-2003 (first entry)
DT

XX DE Human cysteine protease 10.89-encoding cDNA.
 XX KW Human; cysteine protease 10.89; recombinant production; gene therapy;
 KW neuropathy; tumor; cancer; developmental disorder;
 KW embryonic development disorder; immune disorder; inflammatory condition;
 KW cytostatic; antiinflammatory; immunomodulator; gene; ss.
 XX OS Homo sapiens.
 XX FH Key Location/Qualifiers
 FT CDS 20..319
 FT FT /*tag= a
 FT FT /product= "Human cysteine protease 10.89"
 XX PN CM1361276-A.
 XX PD 31-JUL-2002.
 XX PF 26-DEC-2000; 2000CN-00135907.
 XX PR 26-DEC-2000; 2000CN-00135907.
 XX PA (BODE-) BODE GENE DEV CO LTD SHANGHAI.
 XX PI Mao Y, Xie Y;
 XX DR WPI; 2002-751607/82.
 XX DR P-PSDB; ABP58982.
 XX KW Human cysteine proteinase 10.89 polypeptides and polynucleotides encoding
 PT it.
 XX PS Claim 6; Page 25-26 (Disclosure); 32pp; Chinese.
 XX CC The invention relates to human cysteine protease 10.89 (ABP58982) and
 CC nucleic acids encoding it (ABZ70855). The protein has a molecular weight
 CC of 10.89 kD. The invention also relates to a method for the recombinant
 CC production of the protein, an antagonist of the protein, and the use of
 CC the protein, gene and antagonist in therapeutic applications. Cysteine
 CC protease 10.89 can be used in the treatment of a variety of diseases such
 CC as neuropathy, tumor, cancer, developmental disorders (particularly embryonic
 CC development disorders), immune disorders and inflammatory conditions. The
 CC present sequence represents cDNA encoding human cysteine protease 10.89
 XX
 XX SQ Sequence 1222 BP; 392 A; 210 C; 254 G; 366 T; 0 U; 0 Other;
 Query Match 20.8%; Score 166; DB 6; Length 1222;
 Best Local Similarity 65.7%; Pred. No. 9.2e-41;
 Matches 260; Conservative 0; Mismatches 130; Indels 6; Gaps 1;
 QY 380 CTCTCCMAAGCCACGAGAAATTAACTGCTGATATAAAACGTAATTAAGTGAAGAACT 439
 DB 40 CACTCTGCTATGGCACAGGATCAATGCTGATATAAAACATCAATTAATGAGGAGT 99
 QY 440 CGATGCTTGGACAAATAATGAAATAATCTTGAATAATCTTGAAGGAGTGAAGGACC 499
 DB 100 TCGAAAGTTTGGTTCGAAATATGAAAGAAATTTTCATTTTGGTTCGAAAGTTCGAAAGGACC 159
 QY 500 TACTGCAGTCCAGGAGCGATTTTTCGATTCATCATCAAGGAGGAGGAGGATGATGAG 559
 DB 160 TCTGGAGATGAGAAACAGTTTCTGATTTTACCATCAAGGAGGAGGAGGATTTAAAG 219
 QY 560 ACAGAGCTTTTGAACACCTTAAGAGAAACCTGAAACGATGATGATGATGATGATGATG 619
 DB 220 ACAGATCTTAATTCAGTACCTTCGAGAGGTACTAGAAATAAATAATTCACCACTTCA 279
 QY 620 CCTGGAGGATTCACACCCCAATGCAATATCTGTTAATG-----ATTGAGGAGAG 673
 DB 280 CAACACATTAGTCAATCAACAGGAGATCATGTTAGTCAAGACCATGAGAGAA 339
 QY 674 AAAGGATCAGATTCCTGTTTCTTACAAATGAGCAGGATATTCGTAAGTCTCTGCGATA 733

DB 340 AAATGACAAAGTTTCTGCTGTAGCATGGAACAGGATATTGTTGAAGCTCTCTGAATG 399
 QY 734 TGTACCGATCAATAGAGCTTCCAGAGGCTAAGAA 769
 DB 400 TTTGAGTCAAGGAATGCTTTCCAGATGCTAAGAA 435
 RESULT 15
 ADE06992
 ID ADE06992 standard; DNA; 3092 BP.
 XX AC ADE06992;
 XX DT 29-JAN-2004 (first entry)
 XX DE Novel coding sequence (useful for identifying genetic disorders) #58.
 XX KW novel gene; novel protein; tissue marker; molecular weight marker;
 KW chromosome marker; genetic disorder; gene; ds.
 XX OS Unidentified.
 XX PN WO2003054152-A2.
 XX PD 03-JUL-2003.
 XX PF 10-DEC-2002; 2002WO-US039555.
 XX PR 10-DEC-2001; 2001US-0339739P.
 XX PR 11-DEC-2001; 2001US-0339453P.
 XX PR 14-MAR-2002; 2002US-0365091P.
 XX PR 12-APR-2002; 2002US-0372381P.
 XX PR 12-APR-2002; 2002US-0372615P.
 XX PR 22-APR-2002; 2002US-00128558.
 XX PR 24-APR-2002; 2002US-0376045P.
 XX PA (HYSE-) HYSEQ INC.
 XX PI Tang YT, Asundi V, Goodrich RW, Ren F, Zhang J, Zhao QA, Wang J;
 PI Ghosh M, Xue AJ, Wehrman T, Weng G, Zhou P, Drmanac RT, Wang Z;
 PI Ma Y, Wang D, Chen R, Xu C, Boyle BJ;
 XX WPI; 2003-569235/53.
 XX DR P-PSDB; ADE07903.
 XX PT New polynucleotides, useful for expressing recombinant proteins for
 PT analysis, characterization of therapeutic use, or as markers for tissues
 PT in which the corresponding protein is preferentially expressed.
 XX PS Claim 1; SEQ ID NO 58; 1177pp; English.
 XX CC The invention comprises the amino acid and coding sequences of novel
 CC proteins. The DNA and protein sequences of the invention are useful as:
 CC markers for tissues in which the corresponding protein is preferentially
 CC expressed; as molecular weight markers on gels; as chromosome markers or
 CC tags; to identify chromosomes or to map related gene positions; and to
 CC compare with endogenous DNA sequences in patients to identify potential
 CC genetic disorders. The present DNA sequence represents a gene of the
 CC invention.
 XX SQ Sequence 3092 BP; 894 A; 722 C; 726 G; 750 T; 0 U; 0 Other;
 Query Match 19.7%; Score 157.6; DB 9; Length 3092;
 Best Local Similarity 67.8%; Pred. No. 5.9e-38;
 Matches 251; Conservative 0; Mismatches 89; Indels 30; Gaps 1;
 QY 212 TATCAGAGGACATCTATTCCAGCCCAATTCGATTCCTCAGATTCAGTTCCTG 271
 DB 2687 TATCAGAGGATCTTATGCCACCCACCAAGTTCCTCTCTGACCATTCACAG 2746
 QY 272 TTTCCAGCAAGATAGGATGATGCGAGAACTGTTAGCATGCTGTGGGAGAACGT 331

Db	2747	TCTCAGCAAGATGGGCTGATTCAAAAACCTGGTAGTAACGCATTTGTAGGAGGAGCCAA	2806
Qy	332	TACCAGCAGTTTCTCTGGAGATGACCTAGATGCAGAGAAACAGCCTC-----	379
Db	2807	AAACTGCAGTCTCTCCGTAGATGACCAAAAGACCCAGTAGCATCTACTTTGGGAGCTAT	2866
Qy	380	-----CTCTCCAAAGCCAAAGCGAATTAATGCTGATATAAAAG	421
Db	2867	GCCAAATACATTACAAATCACTCCTGTATGGCAAGGAATCAATGCTGATATAAAACA	2926
Qy	422	TAAATTAGTGAAGGAACCTCCGATGCGTTGGACAAAAATATGAAAAATCTTCGAAATGCT	481
Db	2927	TCAATTATGAGGAGTTCGAAAGTTTGGTCGAAATATGAAAGAAATTTTCATTTTCT	2986
Qy	482	TGAAGGAGTGAAGGACCTACTGCAGTCAGGAGGATTTTTCATCCATCAAGGA	541
Db	2987	TGAAGAGTGAAGGACCTCTGGAGATGAAGAAACAGTTTGTGAATTTACCATCAAGGA	3046
Qy	542	AGCAGCAAGA	551
Db	3047	AGCCGCAAGA	3056

Search completed: April 25, 2004, 08:45:45
Job time : 217.564 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 24, 2004, 23:54:27 ; Search time 2106.57 Seconds
(without alignments)
16460.143 Million cell updates/sec

Title: US-10-051-835-12

Perfect score: 800

Sequence: 1 cttctctccagcaggttcag.....taaaagatgtttttttccc 800

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenBank:

1: gb_ba.*
2: gb_hgt.*
3: gb_in.*
4: gb_om.*
5: gb_ov.*
6: gb_pat.*
7: gb_ph.*
8: gb_pl.*
9: gb_pr.*
10: gb_ro.*
11: gb_sts.*
12: gb_sy.*
13: gb_un.*
14: gb_vl.*
15: em_ba.*
16: em_fun.*
17: em_hum.*
18: em_in.*
19: em_ma.*
20: em_om.*
21: em_or.*
22: em_ov.*
23: em_ph.*
24: em_pl.*
25: em_ro.*
26: em_ri.*
27: em_sts.*
28: em_un.*
29: em_vi.*
30: em_hgt_hum.*
31: em_hgt_inv.*
32: em_hgt_other.*
33: em_hgt_mus.*
34: em_hgt_pin.*
35: em_hgt_rtd.*
36: em_hgt_mam.*
37: em_hgt_vrt.*
38: em_sv.*
39: em_higo_hum.*
40: em_higo_mus.*
41: em_higo_other.*

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	769	96.1	1048	9	BC028711	BC028711 Homo sapi
2	758.4	94.8	1498	9	AK098689	AK098689 Homo sapi
3	579.2	72.4	177954	9	AC011366	AC011366 Homo sapi
4	579.2	72.4	216067	9	AC008417	AC008417 Homo sapi
5	447.4	55.9	88423	2	AC022624	AC022624 Homo sapi
6	252	31.5	61880	2	AC021135	AC021135 Homo sapi
7	252	31.5	115916	9	AL590618	AL590618 Human DNA
8	252	31.5	115916	9	AL590618	AL590618 Human DNA
9	249.8	31.2	37959	9	BS337333	BS337333 Human DNA
10	248.8	31.1	547	11	HS229C20T	AL032555 H.sapiens
11	248.8	31.1	61880	2	AC021135	AC021135 Homo sapi
12	225.2	28.1	7090	9	HS808260	BS648113 Homo sapi
13	224.8	28.1	69776	9	AL953870	AL953870 Human DNA
14	223.6	27.9	1840	9	AK123209	AK123209 Homo sapi
15	223.6	27.9	3528	6	AX834225	AX834225 Sequence
16	223.6	27.9	3528	9	AK096544	AK096544 Homo sapi
17	223.6	27.9	3812	6	AR235845	AR235845 Sequence
18	223.6	27.9	3812	6	AX702086	AX702086 Sequence
19	223.6	27.9	6823	9	HS804632	AL833319 Homo sapi
20	187.6	23.4	2021	6	BD205409	BD205409 Tumor-ass
21	187.6	23.4	3069	9	HS427811	AJ728111 Homo sapi
22	178.4	22.3	3075	9	AK126202	AK126202 Homo sapi
23	152	19.0	476	11	HS22882T	AL032554 H.sapiens
24	126.6	15.8	1281	10	BC019773	BC019773 Mus muscu
25	99.6	12.4	144896	9	AL391380	AL391380 Human DNA
26	96.6	12.4	168431	2	AC040972	AC040972 Homo sapi
27	96.6	12.1	161	9	HSU31738	U31738 Homo sapien
28	84.2	10.5	144896	9	AL391380	AL391380 Human DNA
29	82	10.2	69776	9	AL953870	AL953870 Human DNA
30	81.2	10.2	209211	10	AC048362	AC048362 Mus muscu
31	70.6	8.8	65042	6	AR235846	AR235846 Sequence
32	70.6	8.8	65042	6	AX702088	AX702088 Sequence
33	69.8	8.7	1738	9	HS801162	AL117626 Homo sapi
34	69.8	8.7	2110	9	AF141326	AF141326 Homo sapi
35	69.8	8.7	2718	6	BD127822	BD127822 Primer fo
36	69.8	8.7	2718	9	AK074946	AK074946 Homo sapi
37	69.8	8.7	2984	9	BC040581	BC040581 Homo sapi
38	69.8	8.7	3398	9	HS804837	AL833524 Homo sapi
39	69.8	8.7	3690	6	AX467719	AX467719 Sequence
40	69.8	8.7	3690	9	AF097645	AF097645 Homo sapi
41	69.8	8.7	3691	6	A94608	A94608 Sequence 1
42	69.8	8.7	3691	6	E37827	E37827 Novel carci
43	69.8	8.7	3691	6	AX019045	AX019045 Sequence
44	69.8	8.7	3692	9	BC039829	BC039829 Homo sapi
45	69.8	8.7	3970	9	AK128795	AK128795 Homo sapi

ALIGNMENTS

RESULT 1	BC028711	Homo sapiens hypothetical protein MGC27005, mRNA (cDNA clone)	1048 bp	linear	PRI 21-OCT-2003
LOCUS	BC028711	MGC:27005 IMAGE:4828274, complete cds.			
DEFINITION	BC028711	Homo sapiens hypothetical protein MGC27005, mRNA (cDNA clone)			
ACCESSION	BC028711	GI:34192071			
VERSION	BC028711.2	GI:34192071			
KEYWORDS	MGC.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
	1 (bases 1 to 1048)				
	Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,				
	Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,				

Pred. No. is the number of results predicted by chance to have a

Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F., Diachenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Schetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullaly, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S.J., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Kettman, M., Madan, A., Rodrigues, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blacklesley, R.W., Touchman, J.W., Green, E.D., Dickinson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzyzanski, M.I., Skalska, U., Smal, D.E., Scherch, A., Schein, J.E., Jones, S.J., and Marra, M.A.

Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences

Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

22388257

12477932

2 (bases 1 to 1048)

Strausberg, R.

Direct Submission

Submitted (29-APR-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA

NIH-MGC Project URL: <http://mgc.ncl.nih.gov>

On Aug 25, 2003 this sequence version replaced gi:20381102.

Contact: MGC help desk

Email: cgabs-x@mail.nih.gov

Tissue procurement: Miklos Palkovits, M.D., Ph.D.

cDNA Library Preparation: Michael J. Brownstein (NHGRI) & Shiraki Toshiyuki and Piero Carninci (RIKEN)

DNA Sequencing by: The I.M.A.G.E.B. Consortium (LLNL)

http://www.systemsbio.org

contact: amadansystemsbiology.org

Anup Madan, Jessica Fahey, Erin Helton, Mark Kettman, Amuradha Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E.B. Consortium/LLNL at: <http://image.llnl.gov>

Series: IRAX Plate: 34 Row: d Column: 10

This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 22749202.

FEATURES

Location/Qualifiers

1..1048

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/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="MGC:27005 IMAGE:4828274"

/tissue_type="Testis"

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/note="Vector: pBluescript"

1..1048

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/db_xref="LocusID:158852"

246..815

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gene

CDS

96.13; Score 769; DB 9; Length 1048;

ORIGIN

Query Match

Best Local Similarity 98.7%; Pred. No. 6.7e-201; Matches 775; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 16 GTCAGGACTTCCAGCACTGAAACCAATGACCGATATAAAACAGAGAGGCTGTAGATCTCTG 75

Db 223 GTCTCTCTCCAGCAAGGAAACAATGCCGATAAACAAGAGAGGCTGTAGATCTCTG 282

QY 76 AACTGTGTTTAAACGTCGCCAGGAATGTGACAGTCTCTGATTCAGAAAAGCAGAGGA 135

Db 283 AACTGTGTTTAAACGTCGCCAGGAATGTGACAGTCTCTGATTCAGAAAAGCAGAGGA 342

QY 136 TGGCCCTGTTGGCAAGGAAACAAGGACGAGGACAGACGCTTATTGCAAGGCTCTGCCATGT 195

Db 343 TGGCCCTGTTGGCAAGGAAACAAGGACGAGGACAGACGCTTATTGCAAGGCTCTGCCATGT 402

QY 196 CCAAGAAAAGAGCTTATGACAGGACATGCTATTCCACCAGGCTTATTCAGATTCCTCAGA 255

Db 403 CCAAGAAAAGAGCTTATGACAGGACATGCTATTCCACCAGGCTTATTCAGATTCCTCAGA 462

QY 256 TTGATGACTTCACTGTTTCCAGCAAGATAGGATGATGAGAAACCTGGTAGCAATGCGAC 315

Db 463 TTGATGACTTCACTGTTTCCAGCAAGATAGGATGATGAGAAACCTGGTAGCAATGCGAC 522

QY 316 CTGTGGAGGAAACGTTTACAGCAGTCTTCTCGAGATGACCTAGATGACAGAGAACAG 375

Db 523 CTGTGGAGGAAACGTTTACAGCAGTCTTCTCGAGATGACCTAGATGACAGAGAACAG 582

QY 376 CCTCTCTCCCAAGGACGAGAAATTAATCTGATATAAAACCTGTAATTAAGTGAAGG 435

Db 583 CCTCTCTCCCAAGGACGAGAAATTAATCTGATATAAAACCTGTAATTAAGTGAAGG 642

QY 436 AACTCCGATCGTTGGCAAAAATATGAAAAATCTTGAATATCTTGAAGGAGTGCAG 495

Db 643 AACTCCGATCGTTGGCAAAAATATGAAAAATCTTGAATATCTTGAAGGAGTGCAG 702

QY 496 GACCTACTGAGTCAGGAGGAGGATTTTGAATCCATCATCAAGGAGGACGAGATGTA 555

Db 703 GACCTACTGAGTCAGGAGGAGGATTTTGAATCCATCATCAAGGAGGACGAGATGTA 762

QY 556 TGAGACGAGACTTTGTTAAGCACCTTAAGAGAAACCTGAAACCTATGATTTGAGATACT 615

Db 763 TGAGACGAGACTTTGTTAAGCACCTTAAGAGAAACCTGAAACCTATGATTTGAGATACT 822

QY 516 TGTCCCTGGAGGATTATCACACCCCAATGCAATCTCGTTAATGATTCAGAGAGAGAAA 675

Db 823 TGTCCCTGGAGGATTATCACACCCCAATGCAATCTCGTTAATGATTCAGAGAGAGAAA 882

QY 676 AGGATCAGATTGCTGTTTCTTACAATGGACGAGATATTCGAAAGTCTCTCGCATATG 735

Db 883 AGGATCAGATTGCTGTTTCTTACAATGGACGAGATATTCGAAAGTCTCTCGCATATG 942

QY 736 TTACCGAATCAATAGCCTTCCAGAGGCTAAGAAATTTCTGTTAGTAAAGAGATGTTCTTT 795

Db 943 TTACCGAATCAATAGCCTTCCAGAGGCTAAGAAATTTCTGTTAGTAAAGAGATGTTCTTT 1002

QY 796 TTCCC 800

Db 1003 TTCCC 1007

RESULT 2

AK098689

LOCUS

DEFINITION Homo sapiens cDNA FLJ25823 fis, clone TST07974.

ACCESSION AK098689

VERSION AK098689.1 GI:21758775

KEYWORDS cllgo capping; fis (full insert sequence).

SOURCE Homo sapiens

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 Oshima, A., Takahashi-Fujii, A., Tanase, T., Imose, N., Takeuchi, K.,

Arita, M., Mushino, K., Yuuki, H., Hara, H., Suzuki, Y., Hata, H., Nakagawa, K., Mizuno, S., Morinaga, M., Kawamura, M., Sugiyama, T., Irie, R., Otsuki, T., Sato, H., Nishikawa, T., Sugiyama, A., Kawakami, B., Nagai, K., Isegai, T. and Sugano, S.
NEDO human cDNA sequencing project
Unpublished
2 (bases 1 to 1498)

TITLE
JOURNAL
REFERENCE

Sugano, S. and Suzuki, Y.
Direct Submission
Submitted (08-JUL-2002) Sumio Sugano, Institute of Medical Science, University of Tokyo, Laboratory of Genome Structure, Human Genome Center, Shirokane-dai, 4-6-1, Minato-Ku, Tokyo 108-8639, Japan
(E-mail: fldcna@ims.u-tokyo.ac.jp, Tel: 81-3-5449-5286, Fax: 81-3-5449-5416)

COMMENT

NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology (RAB); cDNA library construction and 5'-end one pass sequencing: Institute of Medical Science, University of Tokyo, Laboratory of Genome Structure, Human Genome Center; 3'-end one pass sequencing: RAB; clone selection for full insert sequencing: RAB and Helix Research Institute.

FEATURES

source

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/mol_type="mRNA"
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/clone="TST07974"
/tissue="testis"
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/note="cloning vector: pME18SFL3"
91. 660
/note="unnamed protein product"
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SLIAGKAWKAKMTGHALPPSOLDSDIDFTGFKDRMKQKGNAPGVNVTSPF
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PFESIIKEAARCFMERDFVKKLKKLKKMI"

ORIGIN

Query Match 94.8%; Score 758.4; DB 9; Length 1498;
Best Local Similarity 99.2%; Pred. No. 5.5e-198;
Matches 762; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 33 GAAACAATGACCGATAAACAAGAGAGGTGGCTGTAGATCTGAACTGTGTTTAAACGT 92
DB 85 GAAACAATGACCGATAAACAAGAGAGGTGGCTGTAGATCTGAACTGTGTTTAAACGT 144
QY 93 CCCAGGGAATGTGACGCTTCGTATCAGAAAAGGAGAGATGGCCCTGTGGCAAGG 152
DB 145 CCCAGGGAATGTGACGCTTCGTATCAGAAAAGGAGAGATGGCCCTGTGGCAAGG 204
QY 153 AAACAAGGAGCAGGAGACAGCCTTATTCAGGCTTCGCATGTCCAAAGAAAAGAGCTT 212
DB 205 AAACAAGGAGCAGGAGACAGCCTTATTCAGGCTTCGCATGTCCAAAGAAAAGAGCTT 264
QY 213 ATGACAGGACATGCTATTTCACCCAGCAATGGATTCCTAGATTGATCTTCACCTGCT 272
DB 265 ATGACAGGACATGCTATTTCACCCAGCAATGGATTCCTAGATTGATCTTCACCTGCT 324
QY 273 TTTCAGCAAGATAGGATGATGACAGAAACCTGGTAGCAATGACCTGTGGGAGGAAACGTT 332
DB 325 TTTCAGCAAGATAGGATGATGACAGAAACCTGGTAGCAATGACCTGTGGGAGGAAACGTT 384
QY 333 ACCAGAGTTTCTCGGAGATGACCTAGATGACAGAAACAGAGCTCTCTCCCAAGAGC 392
DB 385 ACCAGAGTTTCTCGGAGATGACCTAGATGACAGAAACAGAGCTCTCTCCCAAGAGC 444
QY 393 CAACAGAGAAATTAATGCTGATATAAAGCTAAATAGTGAAGGAACCTCCGATGCGTTGGA 452
DB 445 CAACAGAGAAATTAATGCTGATATAAAGCTAAATAGTGAAGGAACCTCCGATGCGTTGGA 504

QY 453 CAAAATATGAAAAATCTTCGAAATCTTGAAGAGTGCAGGAGACCTACTGCAGTCAGG 512
DB 505 CAAAATATGAAAAATCTTCGAAATCTTGAAGAGTGCAGGAGACCTACTGCAGTCAGG 564
QY 513 AAGCGATTTTGAATCCATCATCAAGAGAGCAGCAAGATGTTATGAGACGAGATTGTT 572
DB 565 AAACGATTTTGAATCCATCATCAAGAGAGCAGCAAGATGTTATGAGACGAGATTGTT 624
QY 573 AAGCACCTTAAAGAGAAAGTGAACGATGATTGAGAACTATTTGCTCCCTGGAGGATTAT 632
DB 625 AAGCACCTTAAAGAGAAAGTGAACGATGATTGAGAACTATTTGCTCCCTGGAGGATTAT 684
QY 633 CACACCCCAATGCAATATCTCGTTAATGATTGAGGAGAGAAAAGGATCAGATTGCTGTT 692
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RESULT 3

AC011366 177954 bp DNA linear PRI 27-FEB-2002
Homo sapiens chromosome 5 clone CTC-568L21, complete sequence.

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

1. 177954
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
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/clone="CTC-568L21"

ORIGIN

Query Match 72.4%; Score 579.2; DB 9; Length 177954;
Best Local Similarity 86.2%; Pred. No. 1.1e-148;
Matches 652; Conservative 0; Mismatches 103; Indels 1; Gaps 1;

QY 33 GAAACAATGACCGATAAACAAGAGAGGTGGCTGTAGATCTCTGAACTGTGTTTAAACGT 92
DB 158859 GAAACAATGACCGATAAACAAGAGAGAGGTGGCTGTAGATCTCTGAACTGTGTTTAAACGT 158918

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QY 93 CCCAGGGAATGTGACAGTCCCTTCTGATCAGAAAAGGACAGAGATGGCCCTGTTGGCAAGG 152
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QY 153 AAACAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 212
Db 158979 AAACAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 159038
QY 213 ATGACAGAGACATGCTATTCCACCAAGCAATTTGATTTCTCAGATTGATGACTTCACTGGT 272
Db 159039 ATGACAGAGAGATGCTATTCCACCAAGCAATTTGATTTCTCAGATTGATGACTTCACTGGT 159098
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QY 333 ACCAGCAGTTTCTCTGGAGATGACCTAGAAATGACAGAGAAAGAGAGAGAGAGAGAGAGAG 392
Db 159159 ACCAGCAATTTCTCTGGAGATGACCTAGAAATGACAGAGAAAGAGAGAGAGAGAGAGAGAG 159218
QY 393 CAACGAGAAATTAATGCTGATATAAAGCTAAATTAATTAATTAATTAATTAATTAATTAATTA 452
Db 159219 CAAGAAGAAATTAATGCTGATATAAAGCTAAATTAATTAATTAATTAATTAATTAATTAATTA 159278
QY 453 CAAGAATATCAAAATCTTCCAGATGCTTGAAGAGTCCAGAGTCCAGAGTCCAGAGTCCAGAG 512
Db 159279 CGAAATATGAAATCTTCCAGATGCTTGAAGAGTCCAGAGTCCAGAGTCCAGAGTCCAGAGTCC 159338
QY 513 AAGCGATTTTGAATFCAATCATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 572
Db 159339 AAGCGATTTTGAATFCAATCATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 159398
QY 573 AAGCAGCTTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 632
Db 159399 AAGCAGCTTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 159458
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Db 159459 CTCACCGCAATATGATATCTGTTAATGATGAGGA-GAGAGAGAGAGAGAGAGAGAGAGAGAG 159518
QY 692 TTCTACATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 751
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QY 752 CCTTCAGAGGCTAAGAAATTTCTGTTAGTAAAGA 787
Db 159579 CCTTCAGAGGCTAAGAAATTTCTGTTAGTAAAGA 159614

RESULT 4
AC008417/c 216067 bp DNA linear PRI 18-APR-2000
LOCUS Homo sapiens chromosome 5 clone CTC-28708, complete sequence.
DEFINITION AC008417
ACCESSION AC008417
VERSION AC008417.3 GI:6730695
KEYWORDS HG.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 216067)
AUTHORS DOE Joint Genome Institute and Stanford Human Genome Center.
TITLE Direct Submission
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 216067)
AUTHORS DOE Joint Genome Institute.
TITLE Direct Submission
JOURNAL Submitted (03-AUG-1999) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
REFERENCE 3 (bases 1 to 216067)
AUTHORS DOE Joint Genome Center and Stanford Human Genome Center.
TITLE Direct Submission
```

Submitted (22-JAN-2000) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA

4 (bases 1 to 216067)

DOE Joint Genome Institute and Stanford Human Genome Center.

Direct Submission

Submitted (01-FEB-2000) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA

5 (bases 1 to 216067)

DOE Joint Genome Institute and Stanford Human Genome Center.

Direct Submission

Submitted (02-FEB-2000) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA

6 (bases 1 to 216067)

DOE Joint Genome Institute and Stanford Human Genome Center.

Direct Submission

Submitted (15-APR-2000) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA

7 (bases 1 to 216067)

DOE Joint Genome Institute and Stanford Human Genome Center.

Direct Submission

Submitted (18-APR-2000) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA

On Jan 22, 2000 this sequence version replaced gi:6165190.

Draft Sequence Produced by DOE Joint Genome Institute

www.tgi.doe.gov

Finishing Completed at Stanford Human Genome Center

www.shgc.stanford.edu

Quality: Phrap Quality >=40 99.6% of Sequence;

Estimated total Number of Errors is 0.7.

FEATURES

source

1. 216067

/organism="Homo sapiens"

/mol_type="genomic DNA"

/db_xref="taxon:9606"

/chromosome="5"

/clone="CTC-28708"

ORIGIN

Query Match 72.4%; Score 579.2; DB 9; Length 216067;

Best Local Similarity 86.2%; Pred. No. 1.1e-148;

Matches 652; Conservative 0; Mismatches 103; Indels 1; Gaps 1;

QY 33 GAAACATGACCATTAACAG 92

Db 191217 GAAACATGACCATTAACAG 191158

QY 93 CCCAGGGAATGTGACAGTCCCTTCTGATCAGAAAAGGACAGAGATGGCCCTGTTGGCAAGG 152

Db 191157 CCCAGGGAATGTGACAGTCCCTTCTGATCAGAAAAGGACAGAGATGGCCCTGTTGGTAAGG 191098

QY 153 AAACAAG 212

Db 191097 AAACAAG 191038

QY 213 ATGACAGAGATGCTATTCCACCAAGCAATTTGATTTCTCAGATTGATGACTTCACTGGT 272

Db 191037 ATGACAGAGATGCTATTCCACCAAGCAATTTGATTTCTCAGATTGATGACTTCACTGGT 190978

QY 273 TTACACAAAGATAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 332

Db 190977 TGCAGCAAAAGATGGGCTGATGAGAGAACTGCTGTAAGAAATGACCTGTAGGAGGAATCAAT 190918

QY 333 ACCAGCAGTTTCTCTGGAGATGACCTAGAAATGACAGAGAAAGAGAGAGAGAGAGAGAGAG 392

Db 190917 ACCAGCAATTTCTCTGGAGATGACCTAGAAATGACAGAGAAATGACCTGTTCCAAAATGT 190858

QY 393 CAACGAGAAATTAATGCTGATATAAAGCTAAATTAATTAATTAATTAATTAATTAATTAATTA 452

Db 190857 CAACGAGAAATTAATGCTGATATAAAGCTAAATTAATTAATTAATTAATTAATTAATTAATTA 190798

QY 453 CAAGAATATGAAATCTTCCAGATGCTTGAAGAGTCCAGAGTCCAGAGTCCAGAGTCCAGAG 512

Db 190797 CGAAATATGAAATCTTCCAGATGCTTGAAGAGTCCAGAGTCCAGAGTCCAGAGTCCAGAG 190738

QY 513 AAGCGATTTTGAATCCATCATCAAGAGACGACCAAGATGTATGACGAGACTTTGTT 572
 Db 190737 AAATGATTTTGAATCCATCATCAAGAGACGACCAAGATGTATGACGAGACTTTAAT 190678
 QY 573 AAGCACCTTAAGAGAACTCAAGACGTATGATTGAGATCTTGTCCCTGGAGGATTAAT 632
 Db 190677 CAGCACCTTGAAGAACTCGACCAATGATTTCTGGCTACTTGTTCAGAGAGGATCAT 190618
 QY 633 CACACCCCAATGATTAATCTCGTTAATGATGTAGGA-GAGAAAGGATCAGATTGCTGT 691
 Db 190617 CTCACCGCAATGATTAATCTCGTTAATGATGTAGGAGGAGGAGGAGGATCAATTTGCTGT 190558
 QY 692 TTTCTACATCGAGCAGGATATCTGTAAGTCTCTGCGCATCTTACCGAATCAAAATAG 751
 Db 190557 TTTCTAGAAATGAGCAGGATATCTGTAAGTCTCTGAGCTCTAGCATGTTAGTGAATAAATGG 190498
 QY 752 CTTCCAGAGCTAAGAAATTTCTGTAGTAAAGA 787
 Db 190497 CTTCCAGAGCTAAGACATTTCTGTAAAAA 190462

RESULT 5
 AC022624/c
 LOCUS 88423 bp DNA linear HTG 13-JUL-2000
 DEFINITION Homo sapiens clone RP11-24B6, LOW-PASS SEQUENCE SAMPLING.
 ACCESSION AC022624
 VERSION AC022624.2 GI:9129767
 KEYWORDS HTG; HTGS_PHASE0.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 Birren, B., Linton, L., Nusbaum, C. and Lander, E.
 Homo sapiens chromosome, clone RP11-24B6
 Unpublished

2 (bases 1 to 88423)
 Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N.,
 Anderson, S., Baldwin, J., Barna, N., Beckerly, R., Beda, F.,
 Boguslavskiy, L., Boukhgalter, B., Brown, A., Burkett, G., Castle, A.,
 Chepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P.,
 DeArrellano, K., Dewar, K., Domino, M., Doyle, M., Fenestor, J.,
 Ferreira, P., Fitzhugh, W., Forrest, C., Gage, D., Galagan, J.,
 Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L.,
 Howland, J. C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J.,
 Landers, T., Lehoczy, J., Levine, R., Lieu, C., Liu, G., Locke, K.,
 MacDonald, P., Margulis, N., McEwan, P., McGurk, A., McKernan, K.,
 McPheeters, R., Meldrim, J., Meneus, L., Morrow, J., Naylor, J.,
 Norman, C. H., O'Connor, T., O'Donnell, P., Oliver, T. M., Peterson, K.,
 Pierre, N., Pisani, C., Pollara, V., Raymond, C., Riley, R., Rothman, D.,
 Roy, A., Santos, R., Severy, F., Spencer, B., Stange-Thomann, N.,
 Stojanovic, N., Subramanian, A., Talamas, J., Testaye, S., Theodore, J.,
 Tirrell, A., Vassiliev, H., Viel, R., Vo, A., Wu, X., Wyman, D., Ye, W. J.,
 Zimmer, A. and Zody, M.
 Direct Submission

TITLE
 JOURNAL
 COMMENT
 Submitted (06-FEB-2000) Whitehead Institute/MIT Center for Genome
 Research, 320 Charles Street, Cambridge, MA 02141, USA
 On Jul 13, 2000 this sequence version replaced gi:6910695.
 All repeats were identified using RepeatMasker:
 Smit, A.F.A. & Green, P. (1996-1997)
 http://ftp.genome.washington.edu/RM/RepeatMasker.html

----- Genome Center
 Center: Whitehead Institute/ MIT Center for Genome Research
 Center code: WIBR
 Web site: <http://www-seq.wi.mit.edu>
 Contact: sequence_submissions@genome.wi.mit.edu
 ----- Project Information
 Center project name: L4425
 Center clone name: 24_B_6

* NOTE: This record contains 89 individual
 * sequencing reads that have not been assembled into

* contigs. Runs of N are used to separate the reads
 * and the order in which they appear is completely
 * arbitrary. Low-pass sequence sampling is useful for
 * identifying clones that may be gene-rich and allows
 * overlap relationships among clones to be deduced.
 * However, it should not be assumed that this clone
 * will be sequenced to completion. In the event that
 * the record is updated, the accession number will
 * be preserved.

1 944: contig of 944 bp in length
 * 945 1044: gap of 100 bp
 * 1045 1949: contig of 905 bp in length
 * 1950 2049: gap of 100 bp
 * 2050 2954: contig of 905 bp in length
 * 2955 3054: gap of 100 bp
 * 3055 3944: contig of 890 bp in length
 * 3945 4044: gap of 100 bp
 * 4045 4933: contig of 889 bp in length
 * 4934 5033: gap of 100 bp
 * 5034 5921: contig of 888 bp in length
 * 5922 6021: gap of 100 bp
 * 6022 6920: contig of 899 bp in length
 * 6921 7020: gap of 100 bp
 * 7021 7897: contig of 877 bp in length
 * 7898 7997: gap of 100 bp
 * 7998 8903: contig of 906 bp in length
 * 8904 9003: gap of 100 bp
 * 9004 9915: contig of 912 bp in length
 * 9916 10015: gap of 100 bp
 * 10016 10881: contig of 866 bp in length
 * 10882 10981: gap of 100 bp
 * 10982 11886: contig of 905 bp in length
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 * 11987 12876: contig of 890 bp in length
 * 12877 12976: gap of 100 bp
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 * 13852 13951: gap of 100 bp
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 * 14957 15847: contig of 891 bp in length
 * 15848 15947: gap of 100 bp
 * 15948 16860: contig of 913 bp in length
 * 16861 16960: gap of 100 bp
 * 16961 17906: contig of 946 bp in length
 * 17907 18006: gap of 100 bp
 * 18007 18934: contig of 888 bp in length
 * 18935 18994: gap of 100 bp
 * 18995 19913: contig of 919 bp in length
 * 19914 20013: gap of 100 bp
 * 20013 20920: contig of 907 bp in length
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 * 22891 22990: gap of 100 bp
 * 22991 23912: contig of 922 bp in length
 * 23913 24012: gap of 100 bp
 * 24012 24890: contig of 878 bp in length
 * 24891 24990: gap of 100 bp
 * 24991 25869: contig of 879 bp in length
 * 25870 25969: gap of 100 bp
 * 25970 26835: contig of 866 bp in length
 * 26836 26935: gap of 100 bp
 * 26936 27836: contig of 901 bp in length
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 * 27937 28785: contig of 849 bp in length
 * 28786 28885: gap of 100 bp
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 * 29802 29901: gap of 100 bp
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 * 30799 30898: gap of 100 bp
 * 30899 31808: contig of 910 bp in length
 * 31809 31908: gap of 100 bp

* 31909: contig of 886 bp in length
* 32795: gap of 100 bp
* 32796: contig of 886 bp in length
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* 32896: gap of 100 bp
* 33775: contig of 891 bp in length
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* 34766: contig of 886 bp in length
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* 35752: contig of 881 bp in length
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* 36833: contig of 901 bp in length
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* 37335: contig of 864 bp in length
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* 41692: contig of 923 bp in length
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* 43734: contig of 855 bp in length
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* 45786: contig of 878 bp in length
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* 46664: contig of 875 bp in length
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* 46765: contig of 875 bp in length
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* 47740: gap of 100 bp
* 48336: contig of 880 bp in length
* 48337: gap of 100 bp
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* 49716: contig of 901 bp in length
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* 50684: contig of 913 bp in length
* 51584: gap of 100 bp
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* 52599: contig of 916 bp in length
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* 54639: contig of 878 bp in length
* 54640: gap of 100 bp
* 55617: contig of 902 bp in length
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* 56720: gap of 100 bp
* 57619: contig of 879 bp in length
* 57620: gap of 100 bp
* 57719: contig of 886 bp in length
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* 58598: contig of 886 bp in length
* 58599: gap of 100 bp
* 59584: contig of 896 bp in length
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* 60580: contig of 883 bp in length
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* 61563: contig of 904 bp in length
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* 62568: contig of 920 bp in length
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* 63598: contig of 920 bp in length
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* 65593: contig of 905 bp in length
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* 66889: contig of 907 bp in length
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* 67596: contig of 862 bp in length
* 67696: gap of 100 bp

* 68558 68657: gap of 100 bp
* 68658 69515: contig of 858 bp in length
* 69516 69515: gap of 100 bp
* 69516 70472: contig of 857 bp in length
* 70473 70472: gap of 100 bp
Query Match 55.9%; Score 447.4; DB 2; Length 88423;
Best Local Similarity 86.5%; Pred. No. 2.4e-112;
Matches 493; Conservative 0; Mismatches 77; Indels 0; Gaps 0;
QY 33 GAAACAATGACCGATTAACACAGAGAGGTGGCTGTAGATCCTGAACCTGTGTTAAACGT 92
DB 45406 GAAACAATGATGATANAGCAGAGAGGTGCTGTAGACCTGAAATGTTGTTAAACGT 45347
QY 93 CCCAGGGAATGTGACAGTCTTTCATCAAGAAAGGCAGAGGATGGCCCTGTTGGCAAG 152
DB 45346 CCCAGGGAATGTGACAGTCTTTCATCAAGAAAGGCAGAGGATGGCCCTGTTGTTAAG 45287
QY 153 AAACAAGGAGCAGAGACAGCCTTATTCAGAGGCTTCCTCATGTCCTCAAGAAAGAGCCTT 212
DB 45286 AAACAAGGAGCAGAGACAGCCTTATTCAGAGGCTTCCTCATGTCCTCAAGAAAGAGCCTT 45227
QY 213 ATGACAGGACATGCTATTTCACCCAGGCAATTCGATTCTCAGATTGATGACTTCACTGGT 272
DB 45226 ATGACAGGACATGCTATTTCACCCAGGCAATTCGATTCTCAGATTGATGACTTCACTGGT 45167
QY 273 TTCAGCAAGATAGGATGATGCAAAACCTGGTAGCAATGCACCTGTTGGGAGAAACGTT 332
DB 45166 TGCAGCAAGATAGGATGATGCAAAACCTGGTAGCAATGCACCTGTTGGGAGAAACGTT 45107
QY 333 ACCAGCAGTTTCTCTGGAGATGACCTAGATGACAGAGAAACAGCCTCTCTCCCAAAGC 392
DB 45106 ACCAGCAGTTTCTCTGGAGATGACCTAGATGACAGAGAAACAGCCTCTCTCCCAAAGC 45047
QY 393 CAACGAGAAATTAATGCTGATATATAAACCTGTAATAGTGAAGAACTCCGATGCGTTGGA 452
DB 45046 CAGAAGAAATTAATGCTGATATATAAACCTGTAATAGTGAAGAACTCCGATGCGTTGGA 44987
QY 453 CAAAATATGAATAATCTTCGAAATCTTGAAGGATGCAAGGACCTACTGCGAGTCAGG 512
DB 44986 CGAAATATGAATAATCTTCGAAATCTTGAAGGATGCAAGGACCTACTGCGAGTCAGG 44927
QY 513 AAGCGATTTTGAATCCATCATCAAGAGAGCAGCAAGATGTATGACGAGACTTTGTT 572
DB 44926 AATGATTTTGAATCCATCATCAAGAGAGCAGCAAGATTTATGACGAGACTTTAAT 44867
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DB 44866 CAGCAGCTTAAGAGAACTGAAACGTATG 44837

RESULT 6

AC021135 61880 bp DNA linear HTG 07-JUL-2000
LOCUS Homo sapiens chromosome X clone RP11-405J13, WORKING DRAFT
DEFINITION SEQUENCE, 14 unordered pieces.
ACCESSION AC021135
VERSION AC021135.4 GI:8568570
KEYWORDS HTG; HTGS PHASE1; HTGS_DRAFT.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 61880)
AUTHORS Waterston,R.H.
TITLE The sequence of Homo sapiens clone
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 61880)
AUTHORS Waterston,R.H.
TITLE Direct Submission
JOURNAL Submitted (14-JAN-2000) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA

COMMENT

On Jun 16, 2000 this sequence version replaced gi:7109601.

----- Genome Center -----
 Center: Washington University Genome Sequencing Center
 Center code: WUGSC
 Web site: http://genome.wustl.edu/gsc/index.shtml
 ----- Project Information -----
 Center project name: H.NH0405U13
 ----- Summary Statistics -----
 Sequencing vector: M13; 94%
 Chemistry: Dye-terminator ET; 94% of reads
 Chemistry: Dye-terminator Big Dye; 6% of reads
 Assembly program: Phrap; version 0.990319
 Consensus quality: 56291 bases at least Q40
 Consensus quality: 57906 bases at least Q30
 Consensus quality: 59786 bases at least Q20
 Insert size: 222000; agarose-fp
 Insert size: 60580; sum-of-contigs
 Quality coverage: 5.00 in Q20 bases; agarose-fp
 Quality coverage: 5.67 in Q20 bases; sum-of-contigs

* NOTE: This is a 'working draft' sequence. It currently
 * consists of 14 contigs. The true order of the pieces
 * is not known and their order in this sequence record is
 * arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will
 * be preserved.

1 2127: contig of 2127 bp in length
 * 2128 2227: gap of unknown length
 * 2228 3313: contig of 1086 bp in length
 * 3314 3413: gap of unknown length
 * 3414 4919: contig of 1506 bp in length
 * 4920 5019: gap of unknown length
 * 5020 6500: contig of 1481 bp in length
 * 6501 7630: gap of unknown length
 * 7631 7729: contig of 1029 bp in length
 * 7730 10811: contig of 3082 bp in length
 * 10812 10911: gap of unknown length
 * 10912 14705: contig of 3794 bp in length
 * 14706 14805: gap of unknown length
 * 14806 18987: contig of 4182 bp in length
 * 18988 19087: gap of unknown length
 * 19088 23840: contig of 4753 bp in length
 * 23841 23940: gap of unknown length
 * 23941 26787: contig of 2847 bp in length
 * 26788 26887: gap of unknown length
 * 26888 31613: contig of 4726 bp in length
 * 31614 31713: gap of unknown length
 * 31714 38659: contig of 6946 bp in length
 * 38660 38759: gap of unknown length
 * 38760 50631: contig of 11872 bp in length
 * 50632 50731: gap of unknown length
 * 50732 61880: contig of 11149 bp in length.

FEATURES

source

1. 61880
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"
 /chromosome="X"
 /clone="RP11-405U13"

ORIGIN

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 Best Local Similarity 100.0%; Pred. NO. 1.9e-58;
 Matches 252; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 549 AGATGTATGACGAGACTTGTATACCACTTAAGAGAACTGAACCTATGATTGA 608
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 DB 51098 AGATGTATGACGAGACTTGTATACCACTTAAGAGAACTGAACCTATGATTGA 51157

QY 609 GAATACCTGCTCCTGGAGGATTATCACACCCCAATGATATCTCGTTAATGATTGAGG 668
 |||||
 DB 51158 GAATACCTGCTCCTGGAGGATTATCACACCCCAATGATATCTCGTTAATGATTGAGG 51217
 |||||
 QY 669 AGAGAAAAGGATCAGATTGCTGTTTCTACAAATGAGCAGGATATTCTGTAAGTCCTCG 728
 |||||
 DB 51218 AGAGAAAAGGATCAGATTGCTGTTTCTACAAATGAGCAGGATATTCTGTAAGTCCTCG 51277
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 QY 729 GCATATGTTACCAATCAATAGCCTTCAGAGGCTAAGAAATTTCTGTTAGTAAAGAT 788
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 DB 51278 GCATATGTTACCAATCAATAGCCTTCAGAGGCTAAGAAATTTCTGTTAGTAAAGAT 51337
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 QY 789 GTTCTTTTCCC 800
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 DB 51338 GTTCTTTTCCC 51349
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RESULT 7

AL590618

LOCUS

DEFINITION

Human DNA sequence from clone RP13-36C9 on chromosome X, complete

ACCESSION

AL590618

VERSION

AL590618.18

GI:32131111

HTG.

KEYWORDS

SOURCE

ORGANISM

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 115916)

Whithead,S.

Direct Submission

Submitted (20-JUN-2003) Wellcome Trust Sanger Institute, Hinxton,

Cambridgeshire, CB10 1SA, UK. E-mail enquiries:

humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk

On Jun 20, 2003 this sequence version replaced gi:18121499.

During sequence assembly data is compared from overlapping clones.

Where differences are found these are annotated as variations

together with a note of the overlapping clone name. Note that the

variation annotation may not be found in the sequence submission

corresponding to the overlapping clone, as we submit sequences with

only a small overlap as described above.

The following abbreviations are used to associate primary accession

numbers given in the feature table with their source databases:

Emi, EMBL; Swi, SWISSPROT; Tr, TREMBL; Wp, WormPEP; Information

on the WormPEP database can be found at

http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence

was generated from part of bacterial clone contigs of human

chromosome X, constructed by the Sanger Centre Chromosome X Mapping

Group. Further information can be found at

http://www.sanger.ac.uk/HGP/ChrX

RP13-36C9 is from the library RP11-13.1 constructed by the group of

Pieter de Jong. For further details see

http://www.chori.org/bacpac/home.htm

VECTOR: pBAC3.6

----- Genome Center -----

Center: Wellcome Trust Sanger Institute

Center code: SC

Web site: http://www.sanger.ac.uk

Contact: humquery@sanger.ac.uk

This sequence was finished as follows unless otherwise noted: all

regions were either double-stranded or sequenced with an alternate

chemistry or covered by high quality data (i.e., phred quality >=

30); an attempt was made to resolve all sequencing problems, such

as compressions and repeats; all regions were covered by at least

one plasmid subclone or more than one M13 subclone; and the

assembly was confirmed by restriction digest, except on the rare

occasion of the clone being a YAC.

Location/Qualifiers

1. 115916

/organism="Homo sapiens"

source


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/mol type="genomic DNA"
/db xref="taxon:9606"
/chrnosome="X"
/clone="RP13-36C9"
/clone_lib="RPCI-13.1"

ORIGIN
Query Match 31.5%; Score 252; DB 9; Length 115916;
Best Local Similarity 100.0%; Pred. No. 1.8e-58;
Matches 252; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 549 AGATGATGAGACGAGACTTTGTTAGCACCCTTAAGAGAACTGAACGTTATGATTGA 608
Db 29193 AGATGATGAGACGAGACTTTGTTAGCACCCTTAAGAGAACTGAACGTTATGATTGA 29252
QY 609 GAATACCTTGTCCCTGGAGGATTATCACACCCCAATGCAATCTCGTTAAATGATTGAGG 668
Db 29253 GAATACCTTGTCCCTGGAGGATTATCACACCCCAATGCAATCTCGTTAAATGATTGAGG 29312
QY 669 AGAGAAAGATCAGATTGCTGTTTCTTACATGAGAGCAGGATATGCTGGAAGTCTCCTG 728
Db 29313 AGAGAAAGATCAGATTGCTGTTTCTTACATGAGAGCAGGATATGCTGGAAGTCTCCTG 29372
QY 729 GCATATGTTACCGAATCAATAGCCTTCCAGAGCCTTAAGAAATTTCTGTAGTAAAGAT 788
Db 29373 GCATATGTTACCGAATCAATAGCCTTCCAGAGCCTTAAGAAATTTCTGTAGTAAAGAT 29432
QY 789 GTTCTTTTTCCT 800
Db 29433 GTTCTTTTTCCT 29444

RESULT 8
AL590618/c AL590618 115916 bp DNA linear PRI 20-JUN-2003
LOCUS Human DNA sequence from clone Rpl3-36C9 on chromosome X, complete
DEFINITION
ACCESSION AL590618 GI:32131111
VERSION AL590618.18
KEYWORDS HTG.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 115916)
Whitehead, S.
Direct Submission
Submitted (20-JUN-2003) Wellcome Trust Sanger Institute, Hinxton,
Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
humquerry@sanger.ac.uk
On Jun 20, 2003 this sequence version replaced gi:18121499.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.
The following abbreviations are used to associate primary accession
numbers given in the feature table with their source databases:
Em., EMBL; Sw., SWISSPROT; Tr., TREMBL; Wp., WORMPEP; Information
on the WORMPEP database can be found at
http://www.sanger.ac.uk/projects/c_elegans/wormpep
This sequence
was generated from part of bacterial clone contigs of human
chromosome X, constructed by the Sanger Centre Chromosome X Mapping
Group. Further information can be found at
http://www.sanger.ac.uk/HGP/ChrX
RP13-36C9 is from the library RPCI-13.1 constructed by the group of
Pieter de Jong. For further details see
http://www.chori.org/bacpac/home.htm
VECTOR: pBACe3.6
----- Genome Center
Center: Wellcome Trust Sanger Institute
Center code: SC

Web site: http://www.sanger.ac.uk
Contact: humquerry@sanger.ac.uk
-----
This sequence was finished as follows unless otherwise noted: all
regions were either double-stranded or sequenced with an alternate
chemistry or covered by high quality data (i.e., phred quality >=
30); an attempt was made to resolve all sequencing problems, such
as compressions and repeats; all regions were covered by at least
one plasmid subclone or more than one M13 subclone; and the
assembly was confirmed by restriction digest, except on the rare
occasion of the clone being a YAC.
Location/Qualifiers
1. 115916
/organism="Homo sapiens"
/mol type="genomic DNA"
/db xref="taxon:9606"
/chrnosome="X"
/clone="RP13-36C9"
/clone_lib="RPCI-13.1"

FEATURES
source
ORIGIN
Query Match 31.5%; Score 252; DB 9; Length 115916;
Best Local Similarity 100.0%; Pred. No. 1.8e-58;
Matches 252; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 549 AGATGATGAGACGAGACTTTGTTAGCACCCTTAAGAGAACTGAACGTTATGATTGA 608
Db 66875 AGATGATGAGACGAGACTTTGTTAGCACCCTTAAGAGAACTGAACGTTATGATTGA 66816
QY 609 GAATACCTTGTCCCTGGAGGATTATCACACCCCAATGCAATCTCGTTAAATGATTGAGG 668
Db 66815 GAATACCTTGTCCCTGGAGGATTATCACACCCCAATGCAATCTCGTTAAATGATTGAGG 66756
QY 669 AGAGAAAGATCAGATTGCTGTTTCTTACATGAGAGCAGGATATGCTGGAAGTCTCCTG 728
Db 66755 AGAGAAAGATCAGATTGCTGTTTCTTACATGAGAGCAGGATATGCTGGAAGTCTCCTG 66696
QY 729 GCATATGTTACCGAATCAATAGCCTTCCAGAGCCTTAAGAAATTTCTGTAGTAAAGAT 788
Db 66695 GCATATGTTACCGAATCAATAGCCTTCCAGAGCCTTAAGAAATTTCTGTAGTAAAGAT 66636
QY 789 GTTCTTTTTCCT 800
Db 66635 GTTCTTTTTCCT 66624

RESULT 9
BX537333 37959 bp DNA linear PRI 24-JUN-2003
LOCUS Human DNA sequence from clone XX-86277B6 on chromosome X, complete
DEFINITION
ACCESSION BX537333
VERSION BX537333.1 GI:31746321
KEYWORDS HTG.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 37959)
Whitehead, S.
Direct Submission
Submitted (21-JUN-2003) Wellcome Trust Sanger Institute, Hinxton,
Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
humquerry@sanger.ac.uk
Clone requests: clonerequest@sanger.ac.uk
----- Genome Center
Center: Wellcome Trust Sanger Institute
Center code: SC
Web site: http://www.sanger.ac.uk
Contact: humquerry@sanger.ac.uk
-----
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
```

variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest, except on the rare occasion of the clone being a YAC.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em, EMBL; Sw, SWISSPROT; Tr, TREMBL; Wp, WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome X, constructed by the Sanger Centre Chromosome X Mapping Group. Further information can be found at <http://www.sanger.ac.uk/HGP/ChrX> XX-88277B6 is from a Whitehead human fosmid library VECTOR: pEpiFos-5.

FEATURES

source
1. 37959
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="X"
/clone="XX-88277B6"
/clone_lib="Whitehead_fosmid"

ORIGIN

Query Match 31.2%; Score 249.8; DB 9; Length 37959;
Best Local Similarity 97.3%; Pred. No. 7.7e-58;
Matches 254; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 208 AGCTTATGACAGCATGCTATTCCACCAGCCCAATTCGATTCAGATTGATGACTTCA 267
DB 28675 AGCTTATGACAGCATGCTATTCCACCAGCCCAATTCGATTCAGATTGATGACTTCA 28734

QY 268 CTGGTTTCAGCAAGATGATGATGAGCAAAACCTGGTAGCAATGCACCTGTGGAGAA 327
DB 28735 CTGGTTTCAGCAAGATGATGATGAGCAAAACCTGGTAGCAATGCACCTGTGGAGAA 28794

QY 328 AGTTTACCAGAGTTTCTCTGAGATGACCTAGATGACAGAGAAACAGCCCTCTCCCA 387
DB 28795 AGTTTACCAGAGTTTCTCTGAGATGACCTAGATGACAGAGAAACAGCCCTCTCCCA 28854

QY 388 AAAGCCAACGAGAAATTAATGCTGATATAAAACGTAATTAATGTAAGAACTCCGATCGC 447
DB 28855 AAAGCCAACGAGAAATTAATGCTGATATAAAACGTAATTAATGTAAGAACTCCGATCGC 28914

QY 448 TTGGACAAATATGAAAAA 468
DB 28915 TTGGACAAATGTAATATA 28935

RESULT 10
LOCUS HS229C20T 547 bp DNA linear STS 29-OCT-1998
DEFINITION H.sapiens STS from genomic clone 229C20, sequence tagged site.
ACCESSION AL032555
VERSION AL032555.1 GI:3810773
KEYWORDS STS; single read.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 547)
AUTHORS Ross, M., Dunham, A., Huckle, E., Taylor, R. and Hunt, S.
TITLE Direct Submission
JOURNAL Submitted (28-OCT-1998) E-mail contact: humquery@sanger.ac.uk
COMMENT Marker stsG55155 (Primer A : ACCCCAAATGCATAATCTCG; Primer B :

CTTTCAATAAAGCGTTGGG; amplicon size : 184 bp) is from sequence generated from the T7 end of PAC 229C20. 229C20 is part of the bacterial clone contigs constructed by the Chromosome X Mapping Group. (<http://www.sanger.ac.uk/HGP/ChrX/>) 229C20 is from the library constructed at the Roswell Park Cancer Institute by the group of Pieter de Jong.

For further details see <http://bacpac.med.buffalo.edu/>.

FEATURES

Location/Qualifiers
1. 547
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="X"
/clone="229C20"

ORIGIN

Query Match 31.1%; Score 248.8; DB 11; Length 547;
Best Local Similarity 99.2%; Pred. No. 1.8e-57;
Matches 250; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 549 AGATGATGAGACGAGACTTTGTTAAGCACCTTAAGAGAAACTGAACGTATGATTGA 608
DB 262 AGATGATGAGACGAGACTTTGTTAAGCACCTTAAGAGAAACTGAACGTATGATTGA 321

QY 609 GAATACTTGTCCCTGGAGGATATACACCCCAATGCATATCTCTTAATGATTGAGG 668
DB 322 GAATACTTGTCCCTGGAGGATATACACCCCAATGCATATCTCTTAATGATTGAGG 381

QY 669 AGAGAAAGGATCAGATTCTGTTTCTACAATGGAGCAGGATATGCTGAAGTCTCCTG 728
DB 382 AGAGAAAGGATCAGATTCTGTTTCTACAATGGAGCAGGATATGCTGAAGTCTCCTG 441

QY 729 GCATATGTTACCAATCAATAGCCCTTCCAGAGGCTAAGAAATTTCTGTTAGTAAAGAT 788
DB 442 GCATATGTTACCAATCAATAGCCCTTCCAGAGGCTAAGAAATTTCTGTTAGTAAAGAT 501

QY 789 GTTCTTTTTCCTCC 800
DB 502 GTTCTTTTTCCTCC 513

RESULT 11

AC021135/c 61880 bp DNA linear HTG 07-JUL-2000
LOCUS Homo sapiens chromosome X clone RP11-405J13, WORKING DRAFT
DEFINITION SEQUENCE, 14 unordered pieces.

ACCESSION

AC021135 GI:8568570
HTG; HTGS_PHASE1; HTGS_DRAFT.

KEYWORDS

Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (bases 1 to 61880)
Waterston, R.H.
The sequence of Homo sapiens clone

AUTHORS

Unpublished
2 (bases 1 to 61880)
Waterston, R.H.

JOURNAL

Direct Submission
Submitted (14-JAN-2000) Genome Sequencing Center, Washington University School of Medicine, 444 Forest Park Parkway, St. Louis, MO 63108, USA

COMMENT

On Jun 16, 2000 this sequence version replaced gi:7109601.

----- Genome Center -----
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: <http://genome.wustl.edu/gsc/index.shtml>
----- Project Information -----
Center project name: H_NH0405J13
----- Summary Statistics -----
Sequencing vector: M13; 94%

```

Sequencing vector: plasmid; 6%
Chemistry: Dye-primer ET; 94% of reads
Assembly: Dye-terminator Big Dye; 8% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 56291 bases at least Q40
Consensus quality: 57906 bases at least Q30
Consensus quality: 58786 bases at least Q20
Insert size: 222000; agarose-fp
Insert size: 60580; sum-of-contigs
Quality coverage: 5.00 in Q20 bases; agarose-fp
Quality coverage: 5.67 in Q20 bases; sum-of-contigs
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* NOTE: This is a 'working draft' sequence. It currently
* consists of 14 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
*
1
2127: contig of 2127 bp in length
2128: gap of unknown length
2228: contig of 1086 bp in length
3313: contig of 1086 bp in length
3314: gap of unknown length
3413: contig of 1506 bp in length
4919: contig of 1506 bp in length
5019: gap of unknown length
6500: contig of 1481 bp in length
6600: gap of unknown length
7629: contig of 1029 bp in length
7729: gap of unknown length
7730: contig of 3082 bp in length
10911: contig of 3082 bp in length
10912: gap of unknown length
14705: contig of 3794 bp in length
14805: gap of unknown length
18987: contig of 4182 bp in length
19088: gap of unknown length
23840: contig of 4753 bp in length
23941: gap of unknown length
26787: contig of 2847 bp in length
26788: gap of unknown length
31613: contig of 4726 bp in length
31614: gap of unknown length
38659: contig of 6946 bp in length
38759: gap of unknown length
38660: contig of 11872 bp in length
50631: gap of unknown length
50632: gap of unknown length
50731: gap of unknown length
50732: contig of 11149 bp in length.
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FEATURES
    source
        1..61880
            Location/Qualifiers
                /organism="Homo sapiens"
                /mol_type="genomic DNA"
                /db_xref="taxon:9606"
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    polyA_site
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    ORIGIN
        Query Match      31.1%; Score 248.8; DB 2; Length 61880;
        Best Local Similarity 99.2%; Pred. No. 1.4e-57;
        Matches 250; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
    QY 549 AGATGATGAGACGAGACTTTGTTAAGCAGCTTAAGAGAACTGAACGATGATTGA 608
    DB 41284 AGATGATGAGACGAGACTTTGTTAAGCAGCTTAAGAGAACTGAACGATGATTGA 41225
    QY 609 GAATACCTGTGCTGGAGGATTATCACACCCCAATGCATAATCTCGTTAATGATTGAGG 668
    DB 41224 GAATACCTGTGCTGGAGGATTATCACACCCCAATGCATAATCTCGTTAATGATTGAGG 41165
    QY 669 AGAGAAAGATCAGATTGCTGTTTCTACAATGGAGCAGGATATGCTGAAGTCTCCCTG 728
    DB 41164 AGAGAAAGATCAGATTGCTGTTTCTACAATGGAGCAGGATATGCTGAAGTCTCCCTG 41105
    QY 729 GCATATGTTACCGAATCAATAGCCTTCCAGAGGCTAAGAAATTTCTGTTAGTAAAGAT 788

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Db 41104 GCATATGTTACCGAATCAATAGCCTTCCAGAGGCTAAGAAATTTCTGTTAGTAAAGAT 41045
QY 789 GTTCTTTTTCOC 800
Db 41044 GTTCTTTTTCOC 41033
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RESULT 12
HSM808260 HSM808260 7090 bp mRNA linear PRI 30-AUG-2003
LOCUS Homo sapiens mRNA; cDNA DKFZP686E0632 (from clone DKFZP686E0632).
DEFINITION BX648113
ACCESSION BX648113
VERSION BX648113.1 GI:34367272
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 7090)
AUTHORS Ansoorge,W., Krieger,S., Regiert,T., Rittmueller,C., Schwager,B.,
Mewes,H.W., Weil,B., Amid,C., Osanger,A., Fobo,G., Han,M. and
Wiemann,S.
The German Human cDNA Consortium
Direct Submission
Submitted (27-AUG-2003) MIPS, Ingolstaedter Landstr.1, D-85764
Neuherberg, GERMANY
TITLE Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
JOURNAL Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
COMMENT sequenced by EMBL (European Molecular Biology Laboratories,
Heidelberg/Germany) within the cDNA sequencing consortium of the
German Genome Project
This clone (DKFZP686E0632) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de Further
information about the clone and the sequencing project is available
at http://mips.gsf.de/proj/cDNA/.
FEATURES
    source
        1..7090
            Location/Qualifiers
                /organism="Homo sapiens"
                /mol_type="mRNA"
                /db_xref="taxon:9606"
                /clone="DKFZP686E0632"
                /tissue_type="human testis"
                /clone_lib="686 (synonym: hlcc3). Vector pSport1_Sfi; host
                DH10B; sites SfiIA + SfiIB"
                /dev_stage="adult"
    polyA_signal
        7051..7056
    polyA_site
        7073
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        Query Match      28.1%; Score 225.2; DB 9; Length 7090;
        Best Local Similarity 64.8%; Pred. No. 5.1e-51;
        Matches 385; Conservative 0; Mismatches 173; Indels 36; Gaps 2;
    QY 212 TATGACAGGACATGCTATTTCACCCAGCCAAATGGATTTCTCAGATTGATGACTTCACTGG 271
    DB 5731 TATGACAGGACATGCTATTTCACCCAGCCAAATGGATTTCTCAGATTGATGACTTCAAG 5790
    QY 272 TTTTCAGCAAGATAGGATGATGAGAAACCTGGTAGCAATGCACCTGTGGGAGAAACGT 331
    DB 5791 TCTCAGCAAGATAGGCTGATTCAAAACCTGGTAGTACGATTTGTAGAGAGGCCAA 5850
    QY 332 TACCAGCAGTTTCTCTGGAGATGACCTAGAAATGCAGAAACAGCCTC----- 379
    DB 5851 AAACCTGAGTCTCTCCCTAGATGACCAAAAAGACCCAGTAGCATCTACTTTGGGAGCTAT 5910
    QY 380 -----CTCTCCAAAACCCAGCAAAATTAATGCTGATATAAAACG 421
    DB 5911 GCCAAATACATTACAATCACTCTGCTATGGCAGCAAGGATCAATGCTGATATAAACA 5970
    QY 422 TAAATTAGTGAAGGAATCCCGATCGGTTGGACAAAATATGAAAAATCTTGGAAATGCT 481

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Db 5971 TCAATTAATGAGGAAGTTTCGAAAGCTTTGGTCGAAATATGAAGAATTTTCATTTTGGT 6030
QY 482 TGAAGGATGCAAGACCTACTGAGTCAGGAGCGATTTTGAATCCATCATCAAGGA 541
Db 6031 TGAAGAATGCAAGACCTCTGGAGATGAAGAAACAGTTTGTGAATTTACCATCAAGGA 6090
QY 542 AGCACAAGATGTATGAGACGAGACTTTGTTAAGCACCTTAAAGAAACCTGAAACGCTAT 601
Db 6091 AGCCGCAAGGTTTAAAGACGAGTCTTAATTCAGTACCTTGAAGGCTACTAGAAAAAT 6150
QY 602 GATTTGAGATTAATCTGCTCGGAGGATATACACCCCAATATGCAATCTCGTTAATG 661
Db 6151 AAATTTCCACCACTTCAACAACATTAGTCACATCAACAGCAGATCATCATGTTAGT 6210
QY 662 -----ATTGAGCAGAGAAAGCATCAGATTGCTGTTTCTACAAATGAGCAGATATTG 715
Db 6211 CAAAGACAGTGAGAAAAAATGACAAATTTTCTGCTGTAGGATGGAACAGGATATTG 6270
QY 716 CTGAAGTCTCTGGCATATGTTTACCGAATCAAAATAGCCTTCAGAGGCTAAGAA 769
Db 6271 TTGAAGCCTCTGGAATGTTTGAAGTCAAGGGAATGCTTCCAGATGCTAAGAA 6324

RESULT 13
AL953870/c
LOCUS Human DNA sequence from clone RP11-97N5 on chromosome X, complete
DEFINITION
ACCESSION AL953870
VERSION AL953870.2 GI:24527892
KEYWORDS HTG.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 69776)
Heath, P.
Direct Submission
Submitted (01-NOV-2002) Wellcome Trust Sanger Institute, Hinxton,
Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
humquery@sanger.ac.uk
humquery@sanger.ac.uk
On Nov 3, 2002 this sequence version replaced gi:24410492.
----- Genome Center
Center: Wellcome Trust Sanger Institute
Center code: SC
Web site: <http://www.sanger.ac.uk>
Contact: humquery@sanger.ac.uk

During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.
This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em: EMBL; Sw: SWISSPROT; Tr: TrEMBL; Wp: WORMPEP; Information on the WORMPEP database can be found at
http://www.sanger.ac.uk/Projects/C_elegans/wormpep
This sequence was generated from part of bacterial clone contigs of human chromosome X, constructed by the Sanger Centre Chromosome X Mapping Group. Further information can be found at
<http://www.sanger.ac.uk/HGP/ChrX>
RP11-97N5 is from the library RPi-11.1 constructed by the group of Pieter de Jong. For further details see
<http://www.chori.org/bacpac/home.htm>

VECTOR: pBACE3.6.
Location/Qualifiers
1..69776
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosomes="X"
/clone="RP11-97N5"
/clone_lib="RP11-11.1"

ORIGIN
Query Match 28.1%; Score 224.8; DB 9; Length 69776;
Best Local Similarity 93.3%; Pred. No. 5.8e-51;
Matches 235; Conservative 0; Mismatches 17; Indels 0; Gaps 0;
QY 549 AGATGTATGAGACGACCTTTGTTAAGCACCTTAAAGAAACCTGAAACGCTATGATTGA 608
Db 47834 AGATATATGAGCGACACTTTGTTGAGCTCTTGAAGAAACCTGAAACATATGATTGG 47775
QY 609 GAATATCTGCTCGGAGGATATATCAACCCCAATATGCAATCTCTGTTAATGATTGAGG 668
Db 47774 GAGTACTTGTCCATGAGGATATATCACACCCCAATATGCAATCTCTGTTAATGATTCAAG 47715
QY 669 AGAGAAAGGATCAGATTGCTGTTTCTACAAATGAGGAGGATATGCTGAACTCTCCCTG 728
Db 47714 AGAGAAAGGATCAGATTGCTGTTTCTGCAATGAGGAGGATATGCTGAACTCTCCCTG 47655
QY 729 GCATATGTTACCGAATCAAAATAGCCTTCAGAGGCTTAAGAAATTTCTGTTAGTAAAGAT 788
Db 47654 GCATATGTTACTGAATCAAAATGCGCTTCCAGAGCTTAAGAAATTTCTGTTAGTAAAGAT 47595
QY 789 GTTCTTTTCCCC 800
Db 47594 GTTCTTTTCCCC 47583

RESULT 14
AK123209
LOCUS Homo sapiens cDNA FLJ41215 fis clone BRAL22017359, weakly similar
DEFINITION to Homo sapiens RNA helicase HDB/DICE1 mRNA.
ACCESSION AK123209
VERSION AK123209.1 GI:34528699
KEYWORDS oligo capping; fis (full insert sequence).
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
Kawakami, B., Sugiyama, A., Takemoto, M., Sugiyama, T., Irie, R.,
Otsuki, T., Sato, H., Wakamatsu, A., Ishii, S., Yamamoto, J., Isono, Y.,
Kawai-Hio, Y., Saito, K., Nishikawa, T., Kimura, K., Yamashita, H.,
Matsuo, K., Nakamura, Y., Sekine, M., Kikuchi, H., Kanda, K.,
Wagatsuma, M., Murakawa, K., Kanehori, K., Takahashi-Fujii, A.,
Oshima, A., Suzuki, Y., Sugano, S., Nagahara, K., Masuko, Y., Nagai, K.
and Isogai, T.
NEDO human cDNA sequencing project
Unpublished
2 (bases 1 to 1840)
Isogai, T. and Yamamoto, J.
Direct Submission
Submitted (15-JUL-2003) Takao Isogai, FLJ Project (HRI Team); 2-6-7
Kazusa-kamakar, Kisarazu, Chiba 292-0818, Japan
(E-mail: genomics@ri.co.jp, Tel: 81-438-52-3975, Fax: 81-438-52-3986)
NEDO human cDNA sequencing project supported by Ministry of
Economy, Trade and Industry of Japan; cDNA full insert sequencing:
Research Association for Biotechnology (RAB); cDNA library
construction: Helix Research Institute (HRI) (supported by Japan
Key Technology Center etc.); 5' & 3'-end one pass sequencing: RAB,
HRI, and Biotechnology Center, National Institute of Technology and
Evaluation; clone selection for full insert sequencing: HRI and
RAB; annotation: HRI and RAB.
Location/Qualifiers

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1. .1840
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/mol_type="mRNA"
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/clone="BRL22017359"
/tissue_type="alzheimer cortex"
/clone_lib="BRL22"
/notes="cloning vector: pME18SFL3"
47. .973
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VDSLDSDTSLKDLGIQKPGSNFVFGAAXNCSLSDQKDPVASTLGLAMPNTLIQTP
AMAQGINADIHQLMKEVKRFGKRYERIFILIEVQGPFLMKKQFVEFTIKAAARFKR
RVLIQYLEKVLKINSHLHNNINSHNRSSC"

ORIGIN
Query Match 27.9%; Score 223.6; DB 9; Length 1840;
Best Local Similarity 64.6%; Pred. No. 1.5e-50;
Matches 384; Conservative 0; Mismatches 174; Indels 36; Gaps 2;
QY 212 TATGACAGACATGCTATTCCACCAGCCAAATTGGATTCTCAGATTGATGACTTCACCTGG 271
Db 496 TATGACAGAGATCTTATGCCACCCCAACCAAGTGGAATCTCTGTCTGACGACTTCACAAG 555
QY 272 TTTTCAGAAAGATAGATGATGACGAAACCTGTGTAGCAATGACCTGTGGGAGGAAACGT 331
Db 556 TCTCAGCAAGATGGGCTGATTCANAAACCTGGTAGTAACGCAATTTGTAGGAGGACCA 615
QY 332 TACCAGCAGTTTCTCTGGAGATGACCTAGATGACGAGAAACAGCCCTC----- 379
Db 616 AACTGCAGTCTCTCGTAGATGACCAAAAGACCCAGTAGCATCTACTTTGGAGCTAT 675
QY 380 -----CTCTCCAAAAGCCAAACGAGAAATTAATGCTGTATATAAACG 421
Db 676 GCCAAATACATTACAAATCACTCTGCTATGGCACAAGGAATCAATGCTGTATATAAAC 735
QY 422 TAAATTAGTGAAGGAATCCGATGCGTGTGACAAAAATATGAAAAATCTTCGAAATGCT 481
Db 736 TCAATTAAAGAAGAGTTTGAAGTTTGGTCGAAATATGAAGAAATTTTCAATTTGCT 795
QY 482 TGAAGAGTCAAGGACCTACTGCACTGAGGAGGAGGATTTTGAATCCATCATCAAGGA 541
Db 796 TGAAGAAGTCAAGGACCTCTGAGATGAAGAAACAGTTTGTGAAATTTACCATCAAGGA 855
QY 542 AGCAGCAAGATGTATGACGAGACATTTGTTAAGCACCTTTAAGAGAACTGAACGCTAT 601
Db 856 AGCGCAAGGTTTAAAGACGATCTCTAATTCAGTACCTTGAGAGGTAAGTAAAGAAAT 915
QY 602 GATTGAGAAATCTGTCCCTGGAGGATATCAACCCCAATATGCAATATCTCGTTAATG 661
Db 916 AAATTCACCACTTCACAAACATTAAGTACATCAACAGCAGATCATATGTTAGTG 975
QY 662 -----ATTGAGGAGAGAAAGGATCAGATTGCTGTTTCTACAAATGGAGCAGGATATG 715
Db 976 CAAAGACCAATGAGAAAAAATGACAAAGTTTCTGTGCTGTAGATGGAAACAGGATATG 1035
QY 716 CTGAAGTCTCTGGCATATGTTACCGAATCAATAGCCTTCCAGAGGCTTAAGAA 769
Db 1036 TTGAAGCCTCCTGGAATGTTGAGTCAAGGGGATTCCTTTCCAGATGCTTAAGAA 1089
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```
RESULT 15
AX834225
LOCUS
DEFINITION
Sequence 1349 from Patent EP1347046.
ACCESSION
AX834225
VERSION
AX834225.1 GI:39920360
KEYWORDS
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SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 Isogai, T., Sugiyama, T., Otsuki, T., Wakamatsu, A., Sato, H., Ishii, S.,
Yamamoto, J. I., Isono, Y., Hio, Y., Otsuka, K., Nagai, K., Irie, R.,
Tamechika, I., Seki, N., Yoshikawa, T., Otsuka, M., Nagahari, K. and
Masuho, Y.
TITLE Full-length cDNA sequences
JOURNAL Patent: EP 1347046-A 1349 24-SEP-2003;
Research Association for Biotechnology (JP)
FEATURES
source
1. .3528
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
ORIGIN
Query Match 27.9%; Score 223.6; DB 6; Length 3528;
Best Local Similarity 64.6%; Pred. No. 1.5e-50;
Matches 384; Conservative 0; Mismatches 174; Indels 36; Gaps 2;
QY 212 TATGACAGGACATGCTATTCCACCAGCCAAATTGGATTCTCAGATTGATGACTTCACCTGG 271
Db 2178 TATGACAGGAGATCTTATGCCACCCCAACCAAGTGGAATCTCTGTCTGACGACTTCACAAG 2237
QY 272 TTTTCAGCAAGATAGGATGATGACGAAACCTGTGTAGCAATGCACTGTGGGAGGAAACGT 331
Db 2338 TCTCAGCAAGATGGGCTGATTCAAAACTGTGTAGTACGCAATTTGTAGGAGGAGCCAA 2297
QY 332 TACCAGCAGTTTCTCTGGAGATGACCTAGAAATGACAGAAACAGCCCTC----- 379
Db 2298 AAATGCAAGTCTCTCGTAGATGACCAAAAGACCCAGTAGCATCTACTTTGGAGCTAT 2357
QY 380 -----CTCTCCAAAAGCCAAACGAGAAATTAATGCTGTATATAAACG 421
Db 2358 GCCAAATACATTACAAATCACTCTGCTATGGCACAAGGAATCAATGCTGTATATAAAC 2417
QY 422 TAAATTAGTGAAGGAATCCGATGCGTGTGACAAAAATATGAAAAATCTTCGAAATGCT 481
Db 2418 TCAATTAAAGAAGAGTTTGAAGTTTGGTCGAAATATGAAGAAATTTTCAATTTGCT 2477
QY 482 TGAAGGATGCAAGGACCTACTGCACTGAGGAGGAGGATTTTGAATCCATCATCAAGGA 541
Db 2478 TGAAGAAGTCAAGGACCTCTGAGATGAAGAAACAGTTTGTGAAATTTACCATCAAGGA 2537
QY 542 AGCAGCAAGATGTATGACGAGACATTTGTTAAGCACCTTTAAGAGAACTGAACGCTAT 601
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QY 502 GATTGAGAAATCTGTCCCTGGAGGATATCAACCCCAATATGCAATATCTCGTTAATG 661
Db 2598 AAATTCACCACTTCACAAACATTAAGTACATCAACAGCAGATCATCATGTTAGTG 2657
QY 662 -----ATTGAGGAGAGAAAGGATCAGATTGCTGTTTCTACAAATGGAGCAGGATATG 715
Db 2658 CAAAGCAAGTGAAGAAAAAATGACAAAGTTTCTGTGCTGTAGATGGAAACAGGATATG 2717
QY 716 CTGAAGTCTCTGGCATATGTTACCGAATCAATAGCCTTCCAGAGGCTTAAGAA 769
Db 2718 TTGAAGCCTCCTGGAATGTTTGAATCAAGGAAATTCCTTTCCAGATGCTTAAGAA 2771
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Search completed: April 25, 2004, 18:57:33
Job time : 2112.57 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: April 25, 2004, 07:00:48 ; Search time 923.538 Seconds
(without alignments)
16458.288 Million cell updates/sec

Title: US-10-051-835-11

Perfect score: 509

Sequence: 1 gactgtgagggtgtgagg.....agctttctccaaaaaaa 509

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*

1: em_estba:*

2: em_esthum:*

3: em_estin:*

4: em_estmu:*

5: em_estov:*

6: em_estpl:*

7: em_estro:*

8: em_esth:*

9: gb_est1:*

10: gb_est2:*

11: gb_est3:*

12: gb_est4:*

13: gb_est5:*

14: gb_est6:*

15: em_estfun:*

16: em_estom:*

17: em_gss_hum:*

18: em_gss_inv:*

19: em_gss_pln:*

20: em_gss_vrt:*

21: em_gss_fun:*

22: em_gss_imam:*

23: em_gss_imus:*

24: em_gss_pro:*

25: em_gss_rod:*

26: em_gss_phg:*

27: em_gss_vrl:*

28: gb_gss1:*

29: gb_gss2:*

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	509	100.0	570	14	CB994958
2	507.4	99.7	570	14	CB992682
3	502.4	98.7	524	11	AF318372
4	499	98.0	499	12	EG354572

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

5	499	98.0	547	14	N40147	N40147 yw73812.r1
6	481.2	94.5	849	12	EG436305	EG436305 602508742
7	469.4	92.2	520	14	CB961487	CB961487 AGENCOURT
8	432.8	85.0	1176	14	CK230556	CK230556 ILLUMIGEN
9	431.4	84.8	503	9	A1742551	A1742551 wg55c11.x
10	425.8	83.7	429	9	A1189067	A1189067 qd18a09.x
11	419.8	82.5	534	12	EG436468	EG436468 602509139
12	413.8	81.3	430	14	N27023	N27023 yw73812.r1
13	387	76.0	1157	14	CK230595	CK230595 ILLUMIGEN
14	380.4	74.7	394	14	D59091	D59091 HUM521C10B
15	371	72.9	382	13	EX283272	EX283272 BX283272
16	337.4	66.3	756	10	BE903565	BE903565 601677770
17	337.4	66.3	780	10	BE734431	BE734431 601566206
18	335.4	65.9	673	14	CB995986	CB995986 AGENCOURT
19	334	65.6	569	12	EG435916	EG435916 602508269
20	333.6	65.5	453	9	A1189715	A1189715 qd28608.x
21	333.6	65.5	468	9	A1128458	A1128458 qc39a12.x
22	331.6	65.1	496	9	A1188535	A1188535 qd09e11.x
23	331.2	65.1	571	14	N32547	N32547 yw86a06.s1
24	330.6	65.0	468	9	AA039331	AA039331 zk39e06.s
25	329.4	64.7	908	12	EG336433	EG336433 602405375
26	329	64.6	483	9	A1149003	A1149003 qc75a02.x
27	327.6	64.4	496	9	AA993399	AA993399 ct93c08.s
28	326.6	64.2	387	14	T84951	T84951 yd55d10.r1
29	325.4	63.9	592	10	AW972530	AW972530 EST384621
30	322.6	63.4	543	14	N30289	N30289 yw69f02.s1
31	320	62.9	706	10	BE281431	BE281431 601154945
32	318.6	62.6	445	10	BE302172	BE302172 bb92d02.x
33	317.4	62.4	532	9	AA737311	AA737311 nw51g04.s
34	317	62.3	533	14	T87105	T87105 yd88a11.s1
35	316.6	62.2	422	9	AA505794	AA505794 mh98c05.s
36	313	61.5	782	12	EG336384	EG336384 602405325
37	309.8	60.9	437	9	A1740470	A1740470 wg15g08.x
38	309.4	60.8	652	12	EG623213	EG623213 602648125
39	305.4	60.0	982	10	BE900651	BE900651 601673578
40	304.6	59.8	421	9	AA722699	AA722699 zg82c03.s
41	302.4	58.4	588	10	BE733225	BE733225 601568462
42	300	58.9	429	9	A1200158	A1200158 qf97d02.x
43	288.4	56.7	512	14	W93043	W93043 zd93f02.s1
44	280.2	55.0	404	14	H95793	H95793 yv18604.s1
45	273.8	53.8	349	9	A1186558	A1186558 qd21a09.x

ALIGNMENTS

RESULT 1
CB994958
LOCUS
DEFINITION
AGENCOURT 13643389 NIH MGC 148 Homo sapiens cDNA clone
IMAGE:30335086 5', mRNA sequence.
ACCESSION
CB994958
VERSION
CB994958.1 GI:30289478
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
REFERENCE
1 (bases 1 to 570)
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS
NIH-MGC <http://mgc.ncl.nih.gov/>.
TITLE
National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL
Unpublished (1999)
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-r@mail.nih.gov
Tissue Procurement: Dr. Stefan Hansson
CDNA library Preparation: Michael J. Brownstein (NHGRI) with help
and advice from Piero Carninci (RIKEN)
CDNA library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: NDAM356 row: f column: 23

Db 392 CACCTCCTGAGCTGATTGGGCGCTATGCTGGAGCCCGGTGATGAGGAGCCTCAGCAAGAGG 333
 Qy 189 AACCAACCACTGAAAGTCGGGATCCTGCACCTGCTCAGGAGAGAGAAAGATCAGGGTG 248
 Db 332 AACCAACCACTGAAAGTCGGGATCCTGCACCTGCTCAGGAGAGAGAAAGATCAGGGTT 273
 Qy 249 CAGCTGAGACTCAAGTCCCTGACCTGGAAGCTGATCTCCAGGAGCTGCTCAGTCAAAGA 308
 Db 272 CAGCTAAGACTCAAGTCCCTGACCTGGAAGCTGATCTCCAGGAGCTGCTCAGTCAAAGA 213
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 Qy 429 ACAACACAAAACCTGTTTATCTAAGATATTGACTTAAATAATCAAAAATAAATTTTG 488
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 Qy 489 CAGCTTCTCCAAAAAATAA 509
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 clone IMAGE:1724056 3', similar to SW:GG82_HUMAN Q13066 GAGE-2
 PROTEIN. [1] ; mRNA sequence.

A1189067
 A1189067.1 GI:3740276
 EST.
 SOURCE
 Homo sapiens (human)
 ORGANISM
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 429)
 NCBI-CCGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 Unpublished (1997)
 Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 This clone is available royalty-free through LNL ; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.
 Insert Length: 602 Std Error: 0.00
 Seq primer: 40UP from Gibco
 High quality sequence stop: 363.
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 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:1724056"
 /dev_stage="two placentae: one from 8 weeks and another
 from 9 weeks post conception"
 /lab_host="DH10B (ampicillin resistant)"
 /clone_lib="Soares placenta 8to9weeks 2NDHP8to9w"
 /note="Organ: placenta; Vector: p77T3D (Pharmacia) with a
 modified polylinker; Site 1: Not 1; site 2: Eco RI; let
 strand cDNA was primed with a Not I - oligo(dT) primer [5'
 TGTACCAATCTGAAGTGGAGCGCCGCGATTTTATTTTATTTT 3']
 double-stranded cDNA was size selected, ligated to Eco RI
 adaptors (Pharmacia), digested with Not I and cloned into
 the Not I and Eco RI sites of a modified p77T3 vector
 (Pharmacia). Library constructed by Bento Soares and
 M. Fatima Bonaldo."

FEATURES

source
 1..429
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:1724056"
 /dev_stage="two placentae: one from 8 weeks and another
 from 9 weeks post conception"
 /lab_host="DH10B (ampicillin resistant)"
 /clone_lib="Soares placenta 8to9weeks 2NDHP8to9w"
 /note="Organ: placenta; Vector: p77T3D (Pharmacia) with a
 modified polylinker; Site 1: Not 1; site 2: Eco RI; let
 strand cDNA was primed with a Not I - oligo(dT) primer [5'
 TGTACCAATCTGAAGTGGAGCGCCGCGATTTTATTTTATTTT 3']
 double-stranded cDNA was size selected, ligated to Eco RI
 adaptors (Pharmacia), digested with Not I and cloned into
 the Not I and Eco RI sites of a modified p77T3 vector
 (Pharmacia). Library constructed by Bento Soares and
 M. Fatima Bonaldo."

ORIGIN

M. Fatima Bonaldo."

Query Match 83.7%; Score 425.8; DB 9; Length 429;
 Best Local Similarity 99.5%; Pred. No. 2.2e-93;
 Matches 427; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Qy 77 ATGATTTGGCGAGGAGATCAACATATAGGCTTAGGCCGAGGAGAGTGTACCACTCT 136
 Db 429 ATGATTTGGCGAGGAGATCAACATATAGGCTTAGGCCGAGGAGAGTGTACCACTCT 370
 Qy 137 GAGCTGATTTGGCCCTATGCTGGAGCCCGGTGATGAGGAGCCTCAGCAAGAGAACCA 196
 Db 369 GAGCTGATTTGGCCCTATGCTGGAGCCCGGTGATGAGGAGCCTCAGCAAGAGAACCA 310
 Qy 197 ACTGAAAGTCGGGATCTCCCTGCTCAGGAGAGAGAGATCAGGGTGCAGCTGAG 256
 Db 309 ACTGAAAGTCGGGATCTCCCTGCTCAGGAGAGAGAGATCAGGGTGCAGCTGAG 250
 Qy 257 ACTCAAGTGCCTGACCTGGAAGCTGATCTCAGGAGCTGTCTCAGTCAAAGACTGGGGT 316
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 Qy 317 GAATGTGGAATGTGCTCTGATGACCAAGGAGAGATTTCTCCAAAATCAGAACTTTAAA 376
 Db 189 GAATGTGGAATGTGCTCTGATGACCAAGGAGAGATTTCTCCAAAATCAGAACTTTAAA 130
 Qy 377 ATGCCAAGAGGAGGTGACAGGCAACCAAGGTTTAAATGAAGACAAAGCTGAACACACA 436
 Db 129 ATGCCAAGAGGAGGTGACAGGCAACCAAGGTTTAAATGAAGACAAAGCTGAACACACA 70
 Qy 437 AAATGTTTTTATCTAAGATATTGACTTAAATAATCAAAAATAAATTTTTCAGCTTTC 496
 Db 69 AAATGTTTTTATCTAAGATATTGACTTAAATAATCAAAAATAAATTTTTCAGCTTTC 10
 Qy 497 TCCAAAAA 505
 Db 9 TCCAAAAA 1

RESULT 11

EG436468
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 DEFINITION
 602509139F1 NIH_MGC_79 Homo sapiens cDNA clone IMAGE:4619720 5',
 mRNA sequence.
 EG436468
 EG436468.1 GI:13342974
 EST.
 SOURCE
 Homo sapiens (human)
 ORGANISM
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 534)
 NIH-MGC <http://mgs.nci.nih.gov/>.
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: CLONTECH Laboratories, Inc.
 cDNA Library Preparation: CLONTECH Laboratories, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
<http://image.llnl.gov>
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 High quality sequence stop: 523.
 Location/Qualifiers
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 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:4619720"
 /lab_host="DH10B (T1 phage-resistant)"
 /clone_lib="NIH MGC 79"
 /note="Organ: placenta; Vector: pDNR-LIB (Clontech) ;

FEATURES

source
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 /mol_type="mRNA"
 /db_xref="taxon:9606"
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 /lab_host="DH10B (T1 phage-resistant)"
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